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1 795.8 54.7
C 2 699.6 48.1
3 687.4 47.3
4 679.2 46.7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                               Score
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Match Length DB ID
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Copyright (c) 1993 - 2003 Compugen Ltd.
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BM809901 AGENCOURT
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z191b02.s	AA102333		520	29.1		
BM785939 K-EST0064	BM785939	12	452			
BI063672 IL3-UT011	BI063672		437			
Φ.	BI410819		883		436.2	~
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AA290589 zt19c01.s	AA290589		468		438.4	-
BM830577 K-EST0104	BM830577	12	549			_
BI697046 603348915	BI697046	12	758		445.2	٠.
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BM717931 UI-E-EJO-	BM717931	12	457		446	_
AA459626 2x89q01.r	AA459626	9	449	30.8	447.4	~
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	BQ920035	13	951		451.4	_
	BI411732	12	826		470.6	_
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601	BE737427	10	978		479.6	w
	AK009000	H	1338	33.1	481.2	7
	BI085777	12	739	33.2	483.4	01
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BM759571 K-EST0039	BM759571	12	505		492.4	-
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BX283724	BX283724	13	507	34.8	506	
BF034253 601456048	BF034253	10	579		506.6	,,,,
BM837882 K-EST0114	BM837882	12	577	34.9	507.8	0
AA465016 zx80d02.r	AA465016	9	532		508.4	Ψ
K-ESTON6	BM783960	12	525	•	511.4	w
CB050946 NISC 0121	CB050946	14	555	37.3	542.4	7
AW601784 OV4-RT040	AW601784	9	592		566.6	ď
	AI859383	9	727	39.9	580	u
	BE736690	10	1116		8,165	12
6785 NISC not	CB216785	14	614	41.3	600.4	ω
	82899455	10	966	41.3	601	N
wmlofo2 x	AI859367	9	736		619.2	_
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	BG679444	5	686	44.7	650.4	φ
85143 60287069	BI085143	12	793	44.9	652.8	œ
83288 UI-CF-DI	BM983288	12	686	44.9	652.8	~
898352 6016811	BB898352	10	717	46.1	669.6	6
BG469321 602533165	BG469321	10	794	46.3	672.6	u

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## ALIGNMENTS

	COMMENT	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1
Email: Gagabs-remail.nth.gov Tissue Procurement. ATC GNN Library Preparetion: Rubin Laboratory cNN Library Preparetion: Rubin Laboratory DNN sequencing by Agencourt Bloodence Corporation DN sequencing by Agencourt Bloodence Corporation Ecuno distribution: MC Clone distribution information can be found / Lirough the I.M.A.G.E. Consorthum/LLNU at: Place LLCMUSSD.LCOV Place LLCMUSSD.LCOV Place LLCMUSSD.LCOV Dolumn: 04 High quality sequence start: 17	Unpublished Contact: Robert Strausberg, Ph.D.	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 1140)	Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.	Homo sapiens	Homo sapiens (human)	EST.	BM809901.1 GI:19126724	5', mRNA sequence. BM809901	NIH_MGC_98 Homo sapiens cDNA clone	BM809901 1140 bp mRNA linear EST 05-MAR-2002	

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Best Local Similarity

Matches 877; Conserva
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659 ATCACTATCCTGAGCCCTAAGACTGTGAGCTCTGACCCTGGCGTGGTCACCAACAAC 717
689 ATCACTATCCTGAGCCCTAAGACTGTGAGCTCTTCTACCCTGGCGTGGTC-CCAACAAC 747
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                                                                                                         GTCCGGGCCTGCAGCTTCCCTACCGCTGTGCTCAGCCCGGAAACCAGTGCGAGTTGCT
                                                                                                                                                                                  ACGGATGAGCACGATCTCATGTTGCTAAAGCTGGCCAGGGCCCGTAGTGCCGGGGCCCCGC
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GOCACTCC---CALATCCTGCCATGAGAGTCCGCCACCTCCACCTCTCCGCGCCCTCT 140
GCCACTCC----CALATCCTGCCCATGAGAGTCCGCCACCTCCACCTCTCCGCGCCTCT 140
                                                     GCTGGGGCACCACGGCCGCCGGAGAGTGAAGTACAACAAGGGCCTGACCTGCTCCAGC
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Location/Qualifiers
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//alb_host=rpHIOB [phage-resistant)*
//clone_lib="NHIOB [phage-resistant)*
//clone_lib="NHIOB [phage-resistant)*
//clone_lib="NHIOB [phage-resistant)*
RECRI; cDNA made by oligo-dT priming. Directionally __
cloned into Eccell/Yhol sites using the following sy adaptor: GGCACAGAG(G). Library constructed by Ling Hong the laboratory of Gerald M. Rehin (University of lalifornia, Berfeley) using Exp-cnNA synthesis kit (Stretgens) as NHI—GECLIbrary."
156 to 1 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
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0; Mismatches 57;
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	PEATURES source	CASALIPAC LOGALIPAC LOGALIPAC LOGALIPAC LOGALIPAC LOGALIPAC LOGALIPAC LOGALIPAC LOGALIPAC REFERENCE AUTHORS TITLE JOURNAL HEDLINE JOURNAL HEDLINE COMMENT	Db		 D 49	
/organism-Homo sapiens" /mol_type="mank" /mol_type="mank" /mol_type="mank" /cloine="Ul-CF-RNO-dex-h-04-0-Ul" /cloine="Ul-CF-RNO-dex-h-04-0-Ul" /cloine="Ul-CF-RNO-dex-h-04-0-Ul" /cloine="Ul-CF-RNO-dex-h-04-0-Ul" /cloine="Ul-CF-RNO-dex-h-04-0-Ul" /cloine="Ul-CF-RNO-dex-h-04-0-Ul" /cloine="Ul-CF-RNO-dex-h-04-0-Ul" /mole="Ul-CF-RNO-dex-h-04-0-Ul" /mole="Ul-CF-RNO-dex-h-04-0-Ul" /mole="Ul-CF-RNO-dex-h-04-0-Ul" /mole-mole-mole-mole-mole-mole-mole-mole-	Location/Qualifiers 1734	CA11119 UII CCP-RNO-acx-h-04-0-UII 31 MRNA sequence. UII CCP-RNO-acx-h-04-0-UII 31 MRNA sequence. CA111179 CA11179.1 GI:24431277 SST. SST. SST. SST. SST. SST. SST. SS	928 GCCGAACGCCCCATGGTCTCCCAAGGCCACGCCTCGGACGA 968	ACCARGCATCCATTTGGCTCCACCCCAAATCTGCAAATACCTGTCCCCGGGGACAACTAAG		ATGATANTGTGCTGGACTGGACCGGGGCCAGGACCCTTGCCAGAGTGACTCTTGAGGCCCC

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              Homo sapiens (human)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                        BM019631.1 GI:16533985
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CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
BNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LANA at:
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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Plate: LLCM1898 row: m column: 24
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     ACTCGCTCTGTTGTCCATCCCAAGTACCACCAGGGCTCAGGCCCCATCCTGCCAAGGCGA
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Pred. No. 2.2e-128;
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478 ACGGATGAGCACGATCTCATGTTGCTAAAGCTGGCCAGGCCCGTAGTGCCGGGGCCCCGC 537

Query March   46.7%;   Score 679.2;   DB 10;   Length 788;   Best Local Similarity   97.6%;   Fred. No. 9.9-127;   Indols   5;   Gaps   5;   Marches 742;   Conservative   0;   Mismatches   13;   Indols   5;   Gaps   5;   Oy   352   CCANCENGEOGRAFIAGAGATACACCTCCTCTTCTAGAGGAGAGAGAGAGCAGACTCCCC   11	FEATURES Location/Qualifiers  1.758 Source 1.758 Cozgaliams*Nomo apiens* 1.0022013mm*Nomo apiens* 1.0022013mm* 1.0022013mm*Nomo apiens* 1.0022013mm* 1.0022013mm*Nomo apiens* 1.0022013mm* 1.0022		RESULT 4  BG678912  LOCUS  BG678912  BG678912  BG78912  B	
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                                                                                           ACTATCCTGAGCCCTTAAAGAGTGTGAGGTCTACTACCCTGGCGTGGTCA-CAACAACAT 719
                                                                                                                             ACTATCCTGAGCCC-TAAAGAGTGTGAGGTCTTCTACCCTGGCGTGGTCACCACAACAACAT 719
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//lab.hosts_"optnd() (honger-resistant);
/clome_lib="%ilit McC_15"
/clome_lib="%ilit McC_15"
/note="Togan_colon! Vector: pOTBY; Site_1: NbGI, Site_2: Recall; colon! Actor: pOTBY; Site_1: NbGI, Site_2: Recall; colon! Site= using the following 5'
adaptor: GCCACAGG(). Site=salected_5:00bp for average
insert site_1 sib. Library comstructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
Callfornia, Berkeley) using Zah-cank synthesis kit
(Stratageme) and Superscript II RT (Life Technologies)"
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/db_xref="taxon:9606"
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96.7%;
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Pred. No. 2.1e-125;
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CDNA Library Arrayed by: The I.M. A.G. E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics. Inc.
Clone distribution: NGC clone distribution information can be
clone distribution; NGC clone distribution information can be
place: LLCNB19 tow I.M. A.G. E. Consortium/LLNL at: Image.llnl.gov
Plate: LLCNB19 tow I.C. Column: 18
High quality sequence scope: 708.
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Tissue Procurement: DCTD/DTP
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1 (bases 1 to 717)

NIH-McC http://mgc.nci.nih.gov/,
Mational Imstitutes of Health, Mammalian Gene Collection (MGC)
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/mol_type="makk"
/db krei="taxon:9666"
/clone="Myok:199149"
/fisme type="adenocarcinoma cell line"
/clone lib="will MoC_9"
/force="organisme"
/force="or
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                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Meiazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases to 686)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                              (www.openbiosystems.com).
The following repetitive elements were found in sequence: 497-694. ~MIR#SINE/MIR seq primer: M.1 FORWARD FORWARD FORWAYES.
                                                                                                                                                                             Diail paul-incriyekulowa.edu
Tisaue Procurement: Dr. M. J. Welsh, University of Iowa
Tisaue Procurement: Dr. M. J. Welsh, University of Iowa
chan Library preyed by: Dr. M. Bento Soares, University of Iowa
CMA, Library Arrayed by: Dr. M. Bento Soares, University of Iowa
NA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics News.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                McCray Lab
University of Iowa
                                                                                                                                                                                                                                                                                                                                                       8889548
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Genome Res. 6 (9), 791-806 (1996)
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Normalization and subtraction: two approaches to facilitate
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        /tissue_type="Primary Lung
/dev_stage="Adult"
                                   /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="UI-CE-DUI-aav-i-20-0-UI"
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1166 GAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTACTGGGGTCACCCAACCTGACTTCCT 1225
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TGATATAACATGTGTATGTAAATCTTCAT-GTGATTGTCATGTAAGGCTTAACACAGTGG
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//occs_Togon: Lung; Vector: P7773-Pac (Pharmacia) with a //occs_Togon: Lung; Vector: P7773-Pac (Pharmacia) with a modified polylinker; Site 1: Book I; Site 2: Not II; UI-CF-DUI is a normalized cDNA library containing the following tissue(e): Primary Lung Epithalial Cells The library was constructed according to Bonado, Lemon and Soares, Genome Research, 6:791-806, 1956; Pires Errand CDNA synchesis was priced with an oligo-d (DNA mass 1) get of the containing a Nobros. 6:591-806, 1956; Pires Errand CDNA synchesis was priced with Not I. and cloned containing a Nobros. 6:591-806 with Not I. and cloned describanily into p7773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand CDNA contains a library tag sequence that is located between the Not I library is GCCTOTAGC.

TAG_TISSUBLEDING Epithelial Cells Tissue nos 359-368

TAG_TISSUBLEDING Epithelial Cells Tissue nos 359-368

TAG_TISSUBLEDING Epithelial Cells Tissue nos 359-368
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<pre>ECORI; cDNA made by oligo-dT priming. Directional; cloned into EcoRI/KhoI sites using the following 5</pre>	
<pre>/clone_lib="NIH_MGC_98" /note="Organ: brain; Vector: pOTB7; Site 1; XhoI; s</pre>	
<pre>/tissue_type="astrocytoma grade IV, cell line" /lab_host="DH10B (phage-resistant)"</pre>	
/clone="IMAGE:5013670"	
moi type="mRNA"	
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High quality sequence stop: 769.	FEATURES
http://image.llnl.gov plate: LLCM1819 row: 1 column: 23	
Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ELNL)	
Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory	
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov	COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished	JOURNAL
1 (bases 1 to 793) NIH-MGC http://mgc.nci.nih.gov/.	AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
Homo sapiens (human) Homo sapiens	SOURCE
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638 CCCTOTGGCTCTGACCAGCATCCAGCTGTCTACACCCAGATCTGC-AATACATGTCCTGG 716
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599 TCTGGAGGCCCCCCTGGTCTGTACGAGA.-CCTCCAAGGCATCCTCTCGTGGGGTGTTAC 657
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539 GTCACCAACACAACAACGGTGCTGAACTGGACCGGGCCAGAACCCTTGCCAAGGGAAC
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479 ACCTGCTCCAGCATCACTATCCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGGCGTG 538
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602627452P1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752420
mRNA sequence.
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National Instituces of Health, Mammalian Gene Collection (MGC
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Sukaryota, Metazoa, Chordata, Czaniata, Vertebrata, Eureleostomi, Mammalla, Eutheria, Primetes, Catarthini, Hominidae, Homo. 1 (bases 1 to 655) Bonaldo, M.F., Lemmon, G. and Soares, M.B.
                                                                                 BM726274
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EST.
                                                      Homo sapiens (human)
Homo sapiens
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Best Local Similarity
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181 121 847 787 727

ACTGATCCAGATGCTACGCTCAGCTGATCCAGATGTTATGCTCCTGCTGCTGATCCAGATG 966

CCAGCTGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAATAAAGTCATACGCTCC GACGAGACCCTCCAAGGCATCCTCTCGTGGGGTGTTTACCCCTGTGGCTCTGCCCAGCAT GACGAGACCCTCCAAGGCATCCTCTCGTGGGGTGTTTACCCCTGTGGCTCTGCCCAGCAT 846 GCTGGACCGGGGCCAGGACCCTTGCCAGAGTGACTCTGGAGGCCCCCTGGTCTGT GCTGGACTGGACCGGGGCCAGGACCCCTTGCCAGAGTGACTCTGGAGGCCCCCTGGTCTGT 786

CCAGCTGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAATAAAGTCATACGCTCC

180 906 120 60 0

61 ,,

Conservative

0; Mismatches Score 620.8; DB 12; Pred. No. 5.8e-115;

Indels Length 625,

0 Gaps

42.7%;

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mail: benco-searessicowa edu
Tisaue Procurement: Dr. Gregg Hageman
OBNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
DNA Library travyed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this CDNA
Sequence: 498-614, WHIRESIME/MIR
Seq Drimer: M13 Revortes.
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375 Newton Road , 4156 MEBRF, Iowa City,
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                       131
modified polylinker; Site 1, Rope I; Site 2, Not II.

UT-Sado is subtracted CONN library constructed according to Bonaldo, Lennom and Soarce, Genome Research, 6:791-806, 1966, First extrand CONN synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded Only and choned directionally sino pyTT1-Re sis effect; the containing a Not I state or Double stranded only more than 1 the program of the site is freezer; the oligo containing a library peas generally that is forced thereon the Not I site and the double when the sequence tags for this library are: fetal eyes, AGANCHOMA, lens, CGATMAGCOM; eye anterior segment, AATGCOGNI; optic nerve, CCGTMAGCI; retina, CGCGO, Retina Foweal and Macular, GTCC, RFB and Chocold, ACCTA. This library was faced for the program, Gene blaceovery in the Visual System, supported by National By Institute (NEI).*
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/db xref="taxon:9606"
/clone="UI-px00-alh-b-07-0-UI"
/clssue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
choroid"
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//ab_host="DHJDB (Life Technologies) (T1 phage resistant)"
//ab_host="DHJDB (Life Technologies) (T2 phage resistant)"
//clone_lib="U1.E-E30"
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Emmotr: Shock, M.D., bb. D.  CDNN Library Preparation: Life Technologies, Inc.  CDNN Library Preparation: Life Technologies, Inc.  CDNN Library Arrayed by: Greg Lennon, Ph.D.  NN Sequencing by: Washington University Genome Sequencing Centrologies, Contrologies, Contro	,	36) 36) www.ncbi.nlm.nih.gov/nci Institute, Cancer Genome	Ω.	AI859367 736 bp mRNA linear BST 07-MAR-2 wml0f07.xl NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGS:2435547 3 similar to 6W:PSLI_HUMAN 043240 PROTEASE SERINE-LIKE 1 PRECURSON	ACATGTTGTGAGAGACTATGATAT 1351 	CTCTCTGAACCTCAGTTTCCTCATCTGCANATGGGAACAATGACGTGCCTACCTCTTAG	TACCOMACTICATOTOTOCACTOCCCCCCCTTTTTTTTTTTTTTTT	TTATTCCABABAACCAGAMGCCGGTCATCACCCAGCTTCTBABACCAGTTTCTGGG	CCACCTATCCCCATTCTCTGCCTGTACTGAAGCCGAAATGCAGGAAGTGGTGGCAAAGGCGCAACGGCACCTATCCCCATCTGTGCCTGTACTGAAGCTGAAATGCAGGAAGTGGTGGCAAAGGCAAAGGCAAAGGCAAAGGCAAAAAGGCAAAAGGCAAAAGGCAAAAGGCAAAAGGCAAAAGGCAAAAGGCAAAAGGCAAAAGGCAAAAAA	CACTOTTCANACCTCTGCCGCCCTCCACACCTCTANACATCTCCCCCTCTCACCTCATCCCACCTCACCAC	CCAGAGGCTCCATCGTCCATCCTCTTCCTCCCCAGTCGGCTGAACTCTCCCCCTTGTCTC
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SOURCE ORGANISM VERSION KEYWORDS

Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniani; Hominidae; Homo.

ACCESSION DEFINITION

BE899455 BE87. III. 01:10366783

mRNA linear EST 29-SEP-2000 cDNA clone IMAGE:3952448 5',

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Best Local Similarity 92.4%;
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496 CGACTGGCTCTGTTGTCCATCCCAAGTA-CACCAGGCTTCAGGCCCCCATCCTGCCCAAGGC 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 GOGGGGGGGGGGGGGGGGGGGAGGTGGGTGTGCAGGGCTTCGTCCACTGG 295
675 GGGGGCGGGTGGAAGCCTGGGAAGGTCTCGTTCAAGGCCTCTGGTCACTGC 617
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                                                                                                                                                             CCCCTGGTCTGTGACGAGACCCTCCAAGGCATCCTCCTGGGGGTGTTTACCCCTGTGGGC
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                                                                                                                   TCTGCCCAGCATCCAGCTGTCTACACCCCAGATCTGCAAATACATGTCCTGGATCAATAAA 894
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0; Mismatches 53;
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502 CTANAGCTGGCCAGGCCGGTAGTGCCGGGGCCCGGCGCCCTGCAGCTTCCCTAC 561	420 TACCACCAGGGCTCAGGCCCCATCCTGCCAAGGCGAACGGATGAGCACGATCTCATGTTG 479	442 TACCACCAGGGCTCAGGCCCCATCCTGCCAAGGCGAACGGATGAGCACGATCTCATGTTG 501	382 CTGCTTGCTTCTTCSAGGCGACGACCTCCGCGGACGACTCGCTCTGTTGTTCCATCCCAGG 441 361 CTGCTTCTTCSAGGAAGGCAG-TCCGCCGGACCACTCGCTCTGTTGTTCATCCCATCC	322 GTROTRINGCGCCCCCANTROCASANACANGCCACTOTOGCCTCGAGTAGGGARTAGTCA 381 301 GTROTRINGGCCCCCCCACTROCGGAAACANGCCACTOTOGCCTCGAGTAGGGACTGACCAC 360	362 GPCTROCTICTICAACOCCTCCOTTCCACTGCCGCGGGTTGCCTGGTGGACCAAGGTTGG 321 241 GTCTGCCTCTTCAACOGCCTCTGTTCAACTGCCGGGGGGTTGCCTGGTGGACCAAGTTGG 320	202 ACCACTTICAACCCCAAAACCTATROCOCCCCCTTCCCCCCCCCCCCC	142 CTROCOGTTOCTORATOGCOCALACTOTOGGCOCGAGAGGGGGCOCTOCTCCCCALAACGAC 201 121 CTROCOGTTOCTORATOGGCOCALACTCTGGGCCGCAGAGGGGCGTTOCTCCCCCAAAACGAC 201 121 CTROCOGTTOCTORATOGGCOCALACTCTGGGCCGCAGAGGGCGCTTOCTCCCCAAAACGAC 180	82 ATRAMAGETCOCACCTECTACCTCTCCCCCCCCTCTGCCCCCCCCCCCCCTCTGCCCAAACTTG	22 GGGCAAAGCAACTTGGGTCCCCTCCTTCCTTCTATCGGCGACTCCCAAATCCTGGCC 81 1 GGGCAAAAGCAACTTGGGTCCCCTCCCTCCTTCCTATCGGCGACTCCCAAATCCTGGCC 60	Onery Match 41.3% Score 601, DB 10; Length 866; Best Local Stanlarity 9.3%, Pred No. 5.7e-11; Indels 14; Gaps 7; Matches 706; Conservative 0; Wismatches 35; Indels 14; Gaps 7;	/db_xref="thacan:9606" /clone="Thaca:952448" /clone="Thaca:952448" /lab_host="Maca:952448" /lab_host="Maca:95248" /l	riace Juchaz A over to cocumit to the property of the property	with-MGC http://mgc.nci.nih.gov/. Netional Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausherg, Ph.D. Email: Outper remail.nih.gov Tissae Eccurement: CDTD/DTP CONN. Library Preparation: Ling Hong/Rubin Laboratory CONN. Library Armayed by: The I.M.A.G.E. Consortium (LLML) DNN Sequencing by Incyte Genemics Consortium (LLML) DNN Sequencing by Incyte Genemics Consortium (LLML) Consortium (LLML) DNN Sequencing by Incyte Genemics Consortium (LLML)

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Query Match 41.3%;
Best Local Similarity 99.0%;
Matches 604; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bmail: gapbs-remail.nih.gov
CDNA Library Preparation.
DNA Library Preparation.
DNA Library Arrayed by: The I. M.A.G.E. Consortium/Libl.
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NSSC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Libl at:
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Plate: LLAM13166 ro
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:5938427"
/sex="female"
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(Aclone lib-") (
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/lab_host="DH10B (T1-resistant)"
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Score 600.4; DB 14; Length 614; Pred. No. 7.5e-111; 0; Mismatches 6; Indels 0;
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                             CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNIL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LhNL at:
http://lmags.llnli.gov
Plate: LLCddd: row: 1 column: 05
Plate: LLCddd: row: 1 column: 05
High quality sequence stop: 647.
Location/Qualities: 647.
                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                       1 (bases 1 to 1116)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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      /organism="Homo sapiens"
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                                                                       AAGTGCCCTCTCTGAACCTCAGTTTCC 1286
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AAGTGCCCTCTCTGAACCTCAGATTTC 685
                                                                                                                                   TGGGGTCACCCAGACTGACTTCCTCTGCCATTCCCCCGCTGTGTGACTTTGGCGCAAGCCA
                                                                                                                                                                    TGGGTCACCCAACCTGACTTCCTCTGCCACTCCCCGCTGTGACTTTG--GGCAAGCC 1259
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Qy 4	Db 4	B 84	Qy 3	Qy 2 Db 6	D 04	Query Match Best Local Matches 67	FEATURES SOURCE SOURCE ORIGIN	JOURNAL COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM
931 GATGAGCACGATCTCATGTTSCTAAAGCTGGCAGGCCCGGTGATGCGGGGGCCCGGGGTC 540 433 GATGAGCACGATCTCATGTTGCTAAAGCTGGCCAGGCCCGGTAGTGCCGGGGGCCCGGGTC 374	421 GGCTCTGTTGTCCATGCCAAGTACCACAGGCTGAGCCCATCCTGCCAAGACGAACC 480 493 GGCTCTGTTGTCCATGACAAGTACCACCAGGAGCTGAGCCATCCTGCCAAGACGAACC 434	361 GETCOACTAGGGARTGAPCACCTGCTTGCTGCTGCGGGGGGGGGGGGGGGGGGG	301 GTCCTGGTGGACCAAGGTTGGGTGCTGACCGCCCCCACTCCGGAAAACAAGCCACTGTGG 360	241 GCGGCTCCCAGCCTTGCAGGTCTCCCCTCTTCAACGCCTCCTTCCACTGCCCGGGT 300 667 GGC-GCTNGCAGGCCTGCAGGTCTCCCTTCCTTCACTGCCGGGGT 611	181 GOOFFIGETCOCKAANGGACAGGGGTTTGGACCCCGANGCCTMTGGGGCCCCGTTGGGGG 240 727 GOOFFIGETCOCKAANACAANNINGGCGCCTTTGACGAAANNINGCATGGGCCCCCGTGCCGG 668	y Match 29.98; Score 580; DB 9; Length 727; Local Similarity 91.58; Pred, Mo. 9.7e-107; Local Similarity 91.58; Pred, Mo. 9.7e-107; Indels 7; Gaps 6; hes 671; Conservative 0; Mismatches 55; Indels 7; Gaps 6;	cDNA; cDNA; DNA S: Clone found; www-bi Insert Seq pr: High q	lished ct: Ro	<pre>Nammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 727) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Tancer Genome Anatomy Project (CGAP), Tumor Gene Index</pre>	Ut4 Homo sapiens cDN HUMAN 043240 PROTEASS 999 ) Chordata; Craniata;

	01-10-10-10-10-10-10-10-10-10-10-10-10-1	
	900 ACGCTCCAACTGA 912 13 ACGCTCCAACTGA 1	
14	CCAGCATCCAGCTGTCTACACCCCAGATCTGCAAATACATGTCCTGGATCAATAAAGTCAT	
89		
74		
83	780 GGTCTGTGACGAGACCCTCCAAGGCATCCTCTCGTGGGGTGTTTACCCCCTGTGGCTCTGC	
13		
77	721 ATATGTGCTGGACTGGACC-GGGGCCAGGACCCTTGCCAGAGTGACTCTGGAGGCCCCCT	
19		
72	661 ACTATICCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGGCGTGGTCACCAACAACAACATG	
25	313 TGGGGCACCACGGCCGGCCGGAGAGTGAACTACAACGAGGGCCTGACCTGCTCCAGCATC	
660		_
31,	373 CGGGCCCTGCAGCTTCCCTACCGCTGTGCTCAGCCCGGAGACCAGTGCCAGGTTGCTGGC	
600	541 CGGGCCCTGCAGCTTCCCTACCGCTGTGCTCAGCCCGGAGACCAGTGCCCAGGTTGCTGGC (	

Search completed: November 25, 2003, 07:29:52 Job time: 3311 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model November 25, 2003, 06:34:44; Search time 486 Seconds (44) thout alignments (15) updates/sec

Run on:

Title: Perfect score: Sequence: Scoring table: 

US-10-021-368-2

Searched: Gapop 10.0 , Gapext 1.0 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters:

4380138

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications Nh.\*

Ingniz Applications Nh.\*

Ingniz Application (PCT) With PUB seq: \*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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26.4	30.2	30.6	30.8	30.8	35.0	35.0	35.0	35.0	57.0	99.2	100.0	100.0	100.0	100.0	100.0	Query
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US-09-867-701-5175	US-09-867-701-2781	US-09-867-701-2778	US-09-867-701-5352	US-09-867-701-5635	US-09-954-531-1014	US-09-954-531-611	US-09-867-701-5534	US-09-964-824A-311	US-09-888-615-28	US-10-101-510-78	US-10-097-340-166	US-10-021-368-2	US-10-366-288-51	US-10-301-822-94	US-10-059-579-94	ID
Sequence 5175, Ap	Sequence 2781, Ap	Sequence 2778, Ap	Sequence 5352, Ap	Sequence 5635, Ap	Sequence 1014, Ap		Sequence 5534, Ap		2	Sequence 78, Appl		Sequence 2, Appli	Sequence 51, Appl	Sequence 94, Appl	Sequence 94, Appl	Description

45	44	43	42	41	6	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
203.4	203.4	243.4	256	263.4	267.2	267.2	267.2	274.6	295	302.8	310	319	319	319	329.4	335.6	345,4	352	353	353	353	367	376	376	376	376	376	379.6
14.0	14.0	16.7	17.6	18.1	18.4	18.4	18.4	18.9	20.3	20.8	21.3	21.9	21.9	21.9	22.7	23.1	23.8	24.2	24.3	24.3	24.3	25.2	25.9	25.9	25.9	25.9	25.9	26.1
205	205	267	274	534	283	283	283	292	339	335	577	321	321	321	349	377	359	421	373	373	373	434	396	396	396	396	396	430
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## ALIGNMENTS

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; LENGTH: 1454	; SEQ ID NO 94	; SOFTWARE: PatentIn version 3.1	; NUMBER OF SEQ ID NOS: 136	; PRIOR FILING DATE: 2001-01-26	; PRIOR APPLICATION NUMBER: US 09/771,357	; CURRENT FILING DATE: 2003-02-03	; CURRENT APPLICATION NUMBER: US/10/059,579	PILE REFERENCE: JHU1630-1	; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCE	; APPLICANT: FACKLER, Mary Jo.	; APPLICANT: DAVIDSON, Nancy	; APPLICANT: DOOLEY, William C.	; APPLICANT: EVRON, Ella	, APPLICANT: SUKUMAR, Saraswati	, APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE	; GENERAL INFORMATION:	; Publication No. US20030138783A1	; Sequence 94, Application US/10059579	US-10-059-579-94	RESULT 1	
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; TYPE: DNA; Homo sapiens ; ORGANISM: Homo sapiens US-10-059-579-94 LENGTH: 1454

당 Ś 밁 Ś Query Match 100.0%; Score 1454; Best Local Similarity 100.0%; Pred. No. 0; Matches 1454; Conservative 0; Mismatches 121 GCCCGGGCTCTGGCGAAGCTGCTGCTGCTGATGGCGCAACTCTGGGCCGCAGAGGCG DB 12; Length 1454; 0 Indels ٥, Gaps 180 0

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SEO ID NO 94
LENGTH: 1444
TYPE: DNA
GRGANISH Homo Sapiens
FRATURE:
FRATURE:
NAME/KEY: CDS
JOCATION: 821...(912)
US-10-301.822-49
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US-10-301-822-94
US-10-301-822-94
Sequence 94, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
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CURRENT PELLONG DATE. 2002-11-21
CURRENT PELLONG DATE. 2002-11-21
PRICE APPLICATION WINDER: US 60/339,971
PRICE PELLONG DATE: 2001-12-10
PRICE PELLONG DATE: 2001-12-10
PRICE PELLONG DATE: 2001-12-10
PRICE PELLONG DATE: 2002-03-15
PRICE PELLONG DATE: 2002-03-15
PRICE PELLONG DATE: 2002-03-5-20
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APPLICANT: Merger, Allison
APPLICANT: Guillemetre, Tracy L.
APPLICANT: Gaillemetre, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Machanian John E.
APPLICANT: Tithodeau Sesphen N.
APPLICANT: Tithodeau Sesphen N.
APPLICANT: Tithodeau Sesphen N.
APPLICANT: MINISTRICH MOYEL GENES COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: TITLE AND TITLE OF INVENTION: AND
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                                             CAAAGGTTTATTCCAGGGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTA
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Publication No. US20020106367A1
GENERAL INFORMATION:
APPLICANT: Band, Vimla
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Best Local Similarity
Matches 1454; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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FILING APTE: CURKON PRINTS: CURKON 
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET: 225 Franklin Street
CITY: Botton
STATE: MA
STATE: USA
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FILING DATE: 12-Dec-2001
CLASSIFICATION: <Unknown>
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APELICANT: AMDIHA GAMANARABU
APELICANT: Sebastian MORSES:
APELICANT: Sebastian MORSES:
APELICANT: Sechel B. METERS
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Sequence 79, Application US/10101510

Publication No. U92001044825A11
GENERAL INFORMATION:
APPLICANT: WANG, PIXIM

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APPLICANT: PLOWNAM, GRECORY

APPLICANT: MEYTE, DAVID

APPLICANT: CAREFEEL, SEAN

APPLICANT: CAREFEEL, SEAN

APPLICANT: CAREFEEL, SEAN

APPLICANT: SUBMARANA, SICHA

TITLE OF INVENTOR: NOVEL PROTABES

FILE REFERENCE: 038-007.21.21

CURRENT FLIAND ANTE: 2001-06-26

PRIOR REPLICANTON NUMBER: 05/214.047

PRIOR FILIAND ANTE: 2001-06-26

PRIOR REPLICATION NUMBER: 05/214.047

PRIOR FILIAND ANTE: 2001-06-26

SUBMAR: 98-0110 NOS: 150

SEANTH: 81

PRIOR TITLES

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US-09-888-615-28
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I Sequence 28, Application US/09888615
I Setent Mo. US20020064856A1
GENERAL INFORMATION:
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                                                                     TGTGAGGTCTTCTACCCTGGCGTGGTCACCAACAACATGATATGTGCTGGACTGGACCGG 741
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SEQ ID NO 311
LENGTH: 532
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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 69520-73
CURRENT APPLICATION MYMBER. US/09/964,824A
CURRENT FLING DATE: 2000-09-27
FRIOR REPLICATION MYMBER. US/09/964,023
PRIOR REPLICATION MYMBER. US/06/236,03
PRIOR FILING DATE: 2000-09-26
FRIOR REPLICATION MYMBER: US/06/236,032
FRIOR REPLICATION MYMBER: US/06/236,032
FRIOR REPLICATION MYMBER: US/06/236,032
FRIOR REPLICATION MYMBER: US/06/236,032
FRIOR REPLICATION MYMBER: US/06/236,038
FRIOR REPLICATION MYMBER: US/06/236,038
FRIOR REPLICATION MYMBER: US/06/236,038
FRIOR REPLICATION MYMBER: US/06/236,038
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ORGANISM: Homo sapiens
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                                                                                         CTCTCACCTCATTCCCCCACCTATCCCCCATTCTCTGCCTGTACTGAAGCTGAAATGCAGG 1131
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                                                                  CTCTCACCTCATTCCCCCACCTATCCCCCATTCTCTGCCTGTACTGAAGCTGAAATGCAGG
                                                                                                                                                  CTCTCCCCTTGTCTGCACTGTTCAAACCTCTGCCGCCCTCCACACCTCTAAACATCTCCC
                                                                                                                                                                                                                                  CIGCIGATCCAGATCCCAGAGGCICCATCGICCATCCICTCCCCCAGICGGCIGAA 299
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US-09-954-531-611
; Sequence 611, Application US/09954531
; Patent No. US20020165180A1
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Sequence 5534, Application US/09867701

PRECRY NO. USCO02013272711

GENERAL INFORMATION: FALL A.

APPLICANT: Johnes, Robert

APPLICANT: Johnes, Robert

APPLICANT: Uscones, Robert

APPLICANT: Sounds, Robert

APPLICANT: With Information of Control of Cont
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Best Local Similarity 99.4%;
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480 GAGCAGTTACTGGGGTCA-CCAACCTGACTTCCTCTGCCACTCCCCTGCTGTG 532
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                                                                                                    1192 GAGCAGTTACTGGGGTCACCCAACCTGACTTCCTCTGCCACTCCCCGCTGTGTG 1245
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GAGCAGTTACTGGGGTCA-CCAACCTGACTTCCTCTGCCACTCCCTGCTGTGTG 532
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APPLICANT, Meaver, Zoe

APPLICANT, Meaver, Zoe

APPLICANT, Meaver, Zoe

TITLE OF INVENTION: Process for identifying Anti-Cancer Therapeutic Agents Using Canc

TITLE OF INVENTION: Gene Sets

TITLE REFERENCE: 689200-77

CURRENT PILING DATE: 2002-05-02

PRIOR PRILIAGION MUNBER: US/09/954,531

CURRENT FILING DATE: 2002-05-02

PRIOR PRILIAGION MUNBER: US/60/234,039

PRIOR PRILIAGION MUNBER: US/60/234,059

PRIOR PRILIAGION MUNBER: US/60/234,059

PRIOR PRILIAGION MUNBER: US/60/234,059

PRIOR PRILIAGION MUNBER: US/60/234,059

PRIOR PRILIAGION MUNBER: US/60/234,559

PRIOR PRILIAGION MUNBER: US/60/234,569

PRIOR PRILIAGION MUNBER: US/60/234,567

PRIOR PRILIAGION MUNBER: US/60/234,567
REGULT 11.014
US-09-994-531-1014
US-09-994-531-1014
Sequence 1014, Application US/09954331
Sequence 1014, Deplication US/09954331
Settent No. USS-002016518001
SENERAL INFORMATION:
SENERAL INFORMATION:
APPLICANT: Weaver, Zoe
APPLICANT: Weaver, Zoe
APPLICANT: Weaver, Zoe
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US-09-954-531-611
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Best Local Similarity
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SEQ ID NO 611
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Pred. No. 1.8e-139;
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PITIE OF INVENTOR: Gene Sete

FILE REPERSON: GENE SETE

CIRERNY PAPELLOATION NUMBER: US/60/254.531

CIRERNY PAPELLOATION NUMBER: US/60/233.133

PRIOR FILEND ANTE: 2002-05-02

PRIOR PRIOR APPLICATION NUMBER: US/60/234.009

PRIOR PRIOR PAPELLOATION NUMBER: US/60/234.009

PRIOR PRIOR PRIOR DATE: 2000-05-20

PRIOR PRIOR PAPELLOATION NUMBER: US/60/234.509

PRIOR PRIOR PRIOR DATE: 2000-09-20

PRIOR PRIOR PAPELLOATION NUMBER: US/60/234.567

PRIOR PRIOR PRIOR DATE: 2000-09-22

PRIOR PRIOR PAPELLOATION NUMBER: US/60/234.567

PRIOR PRIOR DATE: 2000-09-22

PRIOR PRIOR DATE: 2000-09-22

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US-09-954-531-1014
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AAGTGGTGGCAAAGGTTTATTCCAGAGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGA 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCTGATCCAGATGCCCAGAGGCTCCATCGTCCATCCTCTCCTCCCCAGTCGGCTGAA 1011
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                                                                                                                                                 AAGTGGTGGCAAAGGTTTATTCCAGAGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGA
                                                                                                                                                                                                                                                                                            CTCTCACCTCATTCCCCCACCTATCCCCATTCTCTGCCTGTACTGAAGCTGAAATGCAGG 419
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Pred. No. 1.8e-139;
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RESULT 12
US-09-867-701-5635/c
                                                                                                                                                    Sequence 5635, Application US/09867701 Patent No. US20020132237A1 GENERAL INFORMATION:
APPLICANT: AGLATE, PAUL A.
APPLICANT: AGNORS, ROBOTL
APPLICANT: HARLICOKE, SUSSAL L.
TITLE DE INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVALIAN CANCER
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RESULT 13
US-09-867-701-5352
Sequence 5322, Application US/09867701
Patent No. US20020132237A1
PATENT NO. US20020132237A1
PAPLICANT: AJARC, PAUL A.
APPLICANT: JONES, Robert
APPLICANT: HATLOCKER, SUSANI L.
APPLICANT HATLOCKER, SUSANI L.
TITLE OF INVENTION: CMPOSITIONS AND METHODS FOR THE THERAPY
FILLR REFERENCE: 22011-497
CURRENT FILLNO DATE: 2001-05-29
MOMBER OF SEQ ID NOS: 10912
MOMBER OF SEQ ID NOS: 10912
MOMBER OF SEQ ID NOS: 10912
SEQ ID NO 5392
LENGTH: 449
US-09-867-701-332
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Ouery Match 30.8%; Score 447.4, DB 10; Length 449; Best Local Similarity 99.8%; Fred, No. 1.7e-121; Indels 0; Matches 449; Conservative 0; Mismatches 1; Indels 0;
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Best Local 9
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CURRENT APPLICATION INNERS: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SPOFTWARE: PaecSEQ for Hindows Version 4.0
SEQ ID NO 5635
LEMOTH: 454
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Local Similarity 99.8%; Pred. No. 8.6e-122;
hes 449; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1042 TGCCGCCCTCCACACCTCTAAACATCTCCCCCTCTCACCTCATCCCCCACCTATCCCCAT 1101
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390 GTCCATCCTCTCCCCAGTCGGCTGAACTCTCCCCTTGTCTGCACTGTTCAAACCTC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               922 PACCETICACTERICCAGATGTTATGCTCCTGCTGATGCGAGATGCCCAGAGCTCCATC
450 TACGCTCCAGCTGATCCAGATGTTATGCTCCTGCTGATCCAGATGCCCAGAGGTCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCCTCATCTGCAAAATGGGAACAATGACGTGCCTACCTCTTAGACATGTTGTGAGGAG
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\$ B \$	750 CCCTTGCCHAAGTGACTCTGGAGGCCCCCCTGGTGTGACGAGACCCTCCAAGGCATCCT 809
Db :	
γ	870 CAAATACATGTCCTGGATCAATAAAGTCATACGCTCCAACTGATCCAGATGCTACGCTCC 929
DЬ	121 CAAATACACGTCCTGGATCAATAAAGTCATACGCTCCAACTGATCCAGATGCTACGCTCC 180
γ	930 AGCTGATCCAGATGTTATGCTCCTGCTGATCCAGATGCCCAGAGGCTCCATCGTCCATCC 989
망	181 AGCTGATCCAGATGTTATGCTCCTGCTGATCCAGATGCCCAAGAGGCTCCATCGTCCATCC 240
Ş	990 TCTTCCTCCCCAGTCGGACTCGAACTCTCCCCTTGTCTGCACTCTTCAAACCTCTGCCGCCC 1049
Db	241 TOTTCCTCCCAGTCGCCTGAACTCTCCCCTTGTCTGCACTGTTCAAACCTCTGCCGCCC 300
8	1050 TOCACACCTCTAAACATCTCCCCTCTCACCTCATTCCCCCACCTATCCCCCATTCTCTGCC 1109
Вb	301 TCCACACCTCTAAACATCTCCCCTCTCACCTCATTCCCCCC
Ωγ	1110 TGTACTGAAGCTGAAATGCAGGAAGTGGTGGCAAAGGTTTATTCCAGAGAAGCCAGGAAG 1169
Db	361 TGTACTGAAGCTGAAATGCAGGAAGTGGTGGCAAAGGTTTATTCCAGAGAAGCCAGGAAG 420
07 1	170
망	421 CCGGTCATCACCCAGCCTCTGAGAGCAGT 449
RESULT 14 US-09-867- Sequence Patent I PATENT PATENT I SEQUENCY PATENT I I I I I I I I I I I I I I I I I I I	NS-010-1278/c  US-09-867-701-2778/c  US-09-867-701-2778/c  Sequence 2778, Application US/09867701  Patent No. USE00202112237A1  Patent No. USE00202112237A1  PAPELICANT: ADDIAGNOSITIONS AND METHODS FOR THE THERAPY  TITLE OF INTENTION: OMDOSITIONS AND METHODS FOR THE THERAPY  FILE OF INTENTION: ADD DIAGNOSIS OF OVARIAN CANCER  FILE REFERENCE: 210211-49: US/09/867.701  CURRENT PAPLICATION NUMBER: US/09/867.701  CURRENT PAPLICATION NUMBER: US/09/867.701  USRENT PAPLICATION NUMBER: US/09/867.701  USRCHUMBER: US/09/867.701  U
Query Match Best Local Sir Matches 468;	ald Similarity 99.41; Score 445.4, DB 10; Length 470; ald Similarity 99.41; pedd No. 6.7e-121; Indels 2; Gaps 2; 468; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
υ Qγ	974 GETCONTOSTOCA TOCTOTTOCTOCCOASTOCACTOSACTOTOCCOTTOSTOCACTOST 1033
ργ	1034 CAAACCTCTGCCGCCCTCCCACACCTCTAAACATCTCCCCCTCTCACCTCACTTCCCCCC
Db	410 CAAACCTCTGCGCCCTCCACACCTCTAAACATCTCCCCCTCTCACCTCATTCCCCCC
Qy	1094 ATCCCCATTCTCCCCTGTACTGAAGCTGAAATGCAGGAAGTGGTGGCAAAGGTTTATTC 1153
Db	350 ATCCCCATTCTCTGCCTGTACTGAAGCTGAAATGCAGGAAGTGGCGAAAGGTTTATTC 291
	CAGAGAAGCCAGGAGAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTACTGGGGTCACCCA
O.O	290 CAGAGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTACTGGGGTCACCCA 231

RESU US-C ; Se ; Pa ; GF

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US-09-867-701-2781/c
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1 Sequence 2781, Application US/09867701
/ Setent No. US20020132237A1
/ CENERAL INFORMATION:
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US-09-867-701-2781
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APPLICANT: AGLACE, Paul A.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: CANOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OWNARIAN CANCER
FILE REFERENCE: 210121.39
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT ELIGIDA DATE: 2001-05-29
UNMER OF SEQ ID NOS: 10912
BOUTHORS: FRANCES
SEQ IT NO 2781
LENGTH: 468
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212 CCNGGNACCCGTCNTCNCCCAGCCTCTGNAGACAGTTNCTGGGGTCACCCAACCTGACT 153
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51 TTAACACAGTGGGTGAGTGAGTTCTGACTAAAGGTTACCTGTTGTCGTGAAA 1
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230 ACCTGACTTCCTCGCCACTCCCTGCTGTGAGCTT-GGCAAGCCAAGTCCCTCTGTG 172
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33 ACTATGATATAACATGTGTATGTAAATCTTCA 2

Search completed: November 25, 2003, 09:06:16 Job time: 491 secs

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540	481 GATGACCACGATCTCATGTTOCTAAACCTGGCCAGGCCCGTAGTGCCGGGGCCCGCGCTC 481 GATGACCACCATCTCATGTTTOCTAAAGCTGGCCAGGCCCCGTGTGCCGGGGCCCGCGCCCCCCTC	ନ ଦ
4 8 0	GGFTTGTTGTCATCCAAGTACCAAGGGTCAGGCCCATCCTGCCAAGGGAAGG	
420	361 GCTCGAGTAGGGGAATGATCGCTGCTTCTTCAGGGGAGAGAGCACCCGCGCGAAGGACT	
360	301 GTCCTGGTGGACCAGAGTTGGGTGCTGACGGCGCACTGCGGAAACAAGCCACTGTGG	₽ ₽
360	301 GTCCTGGTGGACCAGAGTTGGGTGCTGACGGCGCGCGCACTGGGGAAACAAGCCACTGTGG	
300	241 GGGGCTGGGAGCCTGGGAGGTCTGGTCTCAACGGCTCTCGTTCAACGGCGCGGTCGGAGCGCGCGGGGGGTCGCGAGCGCGGGGGGTCTCGGGGAGGCCTGGGGAGGCGGGGGGGG	
240	181 GCGCTGCTCCCCCAAAACGACACGCGCTTGGACCCCGGAGCCTATGGCGCCCCGTGCGCG	
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120	61 GGCGACTCCCAGATCCTGGCCATGAGAGCTCCGCACCTCTCCACCTCTCCGCCGCCTCTGGC	
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y Match Local Sin hes 1454;	SULT 2  18-28-198-2  Sequence 2, Application US/  Fatent No. 5843544  ESERBLI INVENTION MARS  TITLE ON THENETION  AUMRES OF SECURSCES: 11  CORRESPONDENCE ADDRESS. 11  CORRESPONDENCE ADDRESS. 12  ADDRESSES: 715A R.G.  STATE: WA  CONTRY: BOSCON  APPLICATION MARSEN  CONTRY: BOSCON  APPLICATION NAMESEN: PROPY  CONTRY: BY APPLICATION DATA  APPLICATION NAMESEN: PROPY  APPLICATION NAMESEN: PROPY  APPLICATION NAMESEN: PROPY  APPLICATION NAMESEN: PROPY  APPLICATION NAMESEN: OS-  TILING DATE: PROPY  APPLICATION NAMESEN: OS-  TILING DATE: OS-OUTH  APPLICATION NAMESEN: OS-OUTH  TELEPHONE: 617/542-8906  TELEPHONE: 617/542-8906  TELEPHONE: 1575 ABOLD  TELEPHON	1441 1441	1381 1381	1321	1261	1201	1141
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RESULT.
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Sequence 2, Application US/09201038
Patent No. 6153387
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SEQUENCE CHARCTERISTICS:
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APPLICANT: BENG, VIMIA
TITLE OF INVENTION: NUES-1 POLYPEPTIDES, DNA, AND RELATED
TITLE OF INVENTION: NUESULES AND METHODS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                             NAME: CLIATA, BAUL T.

NAME: CLIATA, BAUL T.

REGISTRATION NUMBER: 30.152
REFERENCE, DOCUST NUMBER: 00.39
REJERONE/NUMBER: 01.7542-5070
TELECOMPUNICATION INFONMATION:
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
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COMPUTER: IN PC COMPATIBLE
SOFTMARE: PRICEION DATA:
CURRENT APPLICATION DATA:
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                                                                                                               TCTTMGACATGTTGTGAGGAGACTATGATATAACATGTGTATGTGATATCTTCATGTGATT 1380
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RESULTS

US-09-228-111-672
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Sequence 672, Application US/09328111
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Sequence 672, Application O.

APPLICANT EMANATION Wilson O.

APPLICANT EMANATION Wilson O.

APPLICANT BRANGALI, Steven E.

APPLICANT CARCIA II, Eddie
APPLICANT CARCIA E.

APPLICANT CARCIA II, Eddie
TILLE APPRENCE (C. 1227 II)

MARGER OF ESQ II NOS : 800

EARLIER PLING DATE: 1989-06-10

MARGER OF ESQ II NOS : 800

ENGLIEM: THE CARCIA II, EDDIE
APPLICANT III, EDDIE
APPLICANT II, EDDIE
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COMPUTER RADABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER INM COMPATALE
CONFORMER: DISKETE
CONFORMER: RASEES CAT WINDOWS Version 2.0
CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/08/944,483
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Patent No. 6232456
GENERAL INFORMATION:
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Matches 338;
                             INFORMATION FOR SEQ ID NO:
                                                                                         ATTORNY/AGRY INFORMATION:
NAME: Beocker (heryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/NOCKET NUMBER: 689
TELBEOMMUNICATION: TELBEROMINICATION:
TELBEROM: 847/935-1723
TELEFRAN: 847/935-2623
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APPLICANT: GENANDOS, ENWADD N.
APPLICANT: GRANDOS, ENWADD N.
APPLICANT: GRANDOS, ENWADD N.
APPLICANT: GROSELL, JOHN C.
APPLICANT: GROSELL, JOHN C.
APPLICANT: GROPE, STEVEN D.
APPLICANT: GROPE, GRO
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STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
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                                                                                                                                                                                                                                                  Sequence 8, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
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Best Local Sim
Matches 370;
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LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Local Similarity 55.1%;
les 370; Conservative
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COHEM, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, FRULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEMART, KENT D.
STROUPE, STEVEN D.
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759 GAGTGACTCTGGAGGCCCCCTGGTCTGTACGACACCCTCCAAGGCATCCTCTCGTGGGG
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CCAGGATCCGTGTGCGATCACCCGAAAGCCCTGGTGTCTACACGAAAGTCTGCAAATATGT
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Pred. No. 1.8e-33;
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US-08-944-483-8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1192 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARES: FastESG for Windows Version 2.0
CURRENT APPLICATION DATA:
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ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TOPOLOGY: linear
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STATE: IL
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642 CCTGACCTGCTCCAGCATCACTATCCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGG 701
                                       582 CCAGTGCCAGGTTGCTGGGGCACCACCACGGCCCCCGGAGAGTGAAGTACAACAAGGG 641
                                                                                                                         466 CTCCATCACCTGGGCTGTGCGACCCCTCACCCTCACGCTGTGTCACCTGCTGGCAC
                                                                                                                                                              522 AGTGCCGGGGCCCCGCGTCCGGGCCCTGCACCTTCCCTACCGCTGTGCTCAGCCCGGAGA 581
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ilarity 55.1%,
Conservative
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AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
76
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Pred. No. 5.2e-33;
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222 CTATGGCGCCCCGTGGGCGCGCGCGCTCGCAGCCCTGGCAGGTCTCGCTTCTAACGGCCT 281

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US-09-025-059-2
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  Query Match
Best Local Similarity
Matches 370; Conserv
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Patent No. 6075136
                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEREPAL INFORMATION:
APPLICANT: Arg. V. Tom
APPLICANT: CORT by, Mail C.
APPLICANT: CORT by, Mail C.
APPLICANT: CORT by, Mail C.
APPLICANT: ARGADER, KAIL J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lacy J
REGISTRATION NUMBER: 35,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                            TOPOLOGY: LINELL IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Comparible
OPERATING SYSTEM, DO:
SOFTWARE: PASSED for Windows Version
CURRENT APPLICATION NUMBER: US/09/025,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                         LIBRARY: DUAL TONE: 2723646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                   STRANDEDNESS:
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CITY: Palo Alto
                                                                                                                                                                                     LENGTH: 1314 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                766 CCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAATATGT 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          759 GAGTGACTCTGGAGGCCCCCTGGTCTGTGACGGAGCCCTCCAAGGCATCCTCTCGTGGGG
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  Conservative
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                  11.3%;
  0,
               Score 164; DB 3; Length 1314;
Pred. No. 5.5e-33;
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  Mismatches 290;
  Indels
12,
Gaps
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Patent No. 6525174
GENERAL INFORMATION:
                                                                                                                                             EARLIER
EARLIER
EARLIER
                                                                                                                                                                                                                                            CURRENT
                                                                                                                                                                                             EARLIER
EARLIER
                                                                                                                                                                                                                                                                          APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
            RE APPLICATION NUMBER: 60/048,881
ER FILING DATE: 1,997-06-06
ER FILING DATE: 60/048,880
ER FILING DATE: 1,997-06-06
                                                                                                                                          WY FILMS DAYS: 1998-12-04
BE APELICATION UNMERS: DTUUSS/11422
BE FILMS DAYE: 1998-06-04/08-885
BE APELICATION UNMERS: 60/049.375
BE FILMS DAYE: 1997-06-06/049.375
BE FILMS DAYE: 1997-06-06/049.375
BE FILMS DAYE: 1997-06-06
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APPLICATION NUMBER: 60/048,876
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/205,258
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/ TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-189
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EARLIER FILLNO DATE: 1997-06-06
                                                                                  SEQ ID NO 189
LENGTH: 1292
                                                                                                                                                                                                                                                                                             EARLIER
EARLIER
                                                                                                                                          SOFTWARE: Patentin
                                                                                                                                                                     EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
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BARLIER FILING DATE: 1997-06-06
BARLIER APPLICATION UNMEER: 60/046,915
BARLIER FILING DATE: 1997-06-06
BARLIER APPLICATION UNMEER: 60/049,019
BARLIER APPLING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION UNMBER: 60/048,900
EBRLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
BARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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ER APELICATION WHSEE: 60/046 89

ER FILLNO DATE: 1997-06-06

ER PELLICATION WHSEE: 60/046 962

ER FILLNO DATE: 1997-06-06

ER PELLICATION WHSEE: 60/046 963

ER PELLICATION WHSEE: 60/046 963

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ER PELLICATION WHSEE: 60/046 963
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,897
                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,878
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/070,923
FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/094,65
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/092,92;
FILING DATE: 1998-07-15
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FILE REPERSIVE: PROOFF!

CURRENT PELLING MATE: 1998-12-04

EARLIER APELICATION WINBER: PSY1US99/11422

EARLIER APELICATION WINBER: PSY1US99/11422

EARLIER ETLING MATE: 1998-06-04

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; Sequence 247, Application US/09205258
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Best Local Similarity
                                                                                                                                                                                                                                               APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
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BARLIER APPLICATION NUMBER: 60/092,921
BARLIER FILING DATE: 1998-07-15
BARLIER APPLICATION NUMBER: 60/094,657
BARLIER FILING DATE: 1998-07-30
SAMBER OF SEQ ID MOS: 127-0
SOFTWARE: PREMITIN Ver. 2.0
SEQ ID NO 247
SEQ ID NO 247 RE APPLICATION NUMBER: 60/048,875
REFILING DATE: 1997-06-06
REPLICATION NUMBER: 60/049,374
REFILING DATE: 1997-06-06
REPLICATION NUMBER: 60/048,917
REFILING DATE: 1997-06-06 IR APPLICATION NUMBER: 60/048,970
IR FILLING DATE: 1997-06-06
IR APPLICATION NUMBER: 60/048,972
IR APPLICATION NUMBER: 60/048,916
IR APPLICATION NUMBER: 60/048,916
IR FILLING DATE: 1997-06-06
IR FILLING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,896 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/049,020 APPLICATION NUMBER: 60/048,915 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/049,019 APPLICATION NUMBER: 60/048,899 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,893 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/070,923
FILING DATE: 1997-12-18 FILING DATE: 1997-06-00 APPLICATION NUMBER: 60/048,900 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,901 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,892 APPLICATION NUMBER: 60/048,882 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,884 APPLICATION NUMBER: FILING DATE: 1997-06-06 FILING DATE: 1997-06-06 PILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,877 APPLICATION NUMBER: 60/048,962 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,897 APPLICATION NUMBER: 60/048,883 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,974 APPLICATION NUMBER: 60/048,949 APPLICATION NUMBER: 60/049,373 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,964 APPLICATION NUMBER: APPLICATION NUMBER: 60/048,894 FILING DATE: 1997-06-06 FILING DATE: 1997-06-06 APPLICATION NUMBER: APPLICATION NUMBER: 60/048,878 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,963 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,898 FILING DATE: 1997-06-06 FILING DATE: 1997-06-06 60/048,895 60/048,971 60/048,876

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LOCATION: (37)
OTHER INFORMATION:
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LOCATION: (36)
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LOCATION: (35)
OTHER INFORMATION:
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TYPE: DNA
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                                                      TGTTTACCCCTGTGGCTCTGCCAGCATCCAGCTGTCTACACCCCAGATCTGCAAATACAT 878
                                                                              GGTGACTCGGGGGGCCTCTGGTAACCAGTCTCTTCAAGGCATTATCTCCTGGG
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                                      CCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAATATGT
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Pred. No. 8.3e-33;
2; Mismatches 290; Indels
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US-09-386-642-10
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Best Local S
Matches 359
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RESULT 11
US-09-366-642-10
US-09-366-642
Requence 10, Application US/09386642
Requence 10, Application US/09386642
Retent No. 64201157
GENERAL INFORMATION:
APPLICANT: DAIRON, Andrew
APPLICANT: 04, Jenson
APPLICANT: 04, Jenson
APPLICANT: 04, Jenson
APPLICANT: 05, Jenson
APPLICANT: 05, Jenson
APPLICANT: 05, Jenson
APPLICANT: 06, Jenson
APPLICANT: 07, J
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/ Match 11.1%; Local Similarity 55.4%; les 359; Conservative ( 606 CACCACGGCCGCGGGAGGTGAAGTACAACAAGGGCCTGACCTGCTCCAGCATCACTAT 429 CAATGACATGATGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACC 486 GCACGATCTCATGTTGCTAAAGCTGGCCAGGCCCGTAGTGCCGGGGCCCCGCGTCCGGGC 426 TGTTGTCCATCCCAAGTACCACCAGGCTCAGGCCCCATCCTGCCAAGGCGAACGGATGA 485 318 CCTGGGGCAGCACACCTC-----CAGAAGGAGGAGGGCTGTGAGCAGACCCGGAC 258 CATCGCCCCAGATGGCTCCTGACAGCCCACTGCCTCAAGCCCCGCTACATAGTTCA 306 GGTGGACCAGAGTTGGGTGCTGACGGCCGCCACTGCGGAAACAAGCCACTGTGGGCTCG 198 CTCCCAGCCCTGGCAGGCAGCCCTGTTCGAGAAGACGCGGCTACTCTGTGGGGGCGACGCT 246 CTCGCAGCCCTGGCAGGTCTCGCTCTTCAACGGCCTCTCGTTCCACTGCGCGGGTGTCCT GCATCCAGCTGTCTACACCCCAGATCTGCAAATACATGTCCTGGATCAA 890 CTGTGACGAGACCCTCCAAGGCATCCTCTCGTGGGGTGTTTACCCCTGTGGCTCTGCCCA reccaecerecade a acceptance de la constanción de CCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGGCGTGGTCACCAACAACATGATATG CAGCACGTCCAGCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCAT AMAGCCTGGTGTGTACACGAMAGTCTGCAMATATGTGGACTGGATCCM 836 CIGIAACCAGICICITCAAGGCATTAICITCCIGGGGCCAGGATCCGTGTGCGATCACCCG TGC---TGGACTGGACCGGGGCCAGGACCCTTGCCAGAGTGACTCTGGACGCCCCCTGGT CATTGAGCACCAGAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTG CCTCACCCTCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCCGGCTGGGG AGCCACTGAGTCCTTCCCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCG Score 160.8; DB 4; Pred. No. 3.4e-32; 0; Mismatches 277; Length Indels 12, Gaps 788 842 665 728 999 809 605 548 488 545 428 368 425 317 305

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TELEPHAY, 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
TYPE: nucleic acid
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Best Local :
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CHERENT APPLICATION DATA:
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APPLICANT: GOIL, Surya K.
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
TITLE OF INVENTION: KALLIKREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION: 424
APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
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STREET: 3174 Porter Drive
CITY: Palo Alto
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                594 TGCTGGCTGGGCACCACGGCGCCCCGGAGAGTGAAGTACAAGAAGAGCCTGACCTGCTC 653
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                                                                                347 CARAGACCACCGCARTGACATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTG 406
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APPLICANT: DAXYOW, Andrew
APPLICANT: Q1, Jenson
APPLICANT: Andrade-Gordon, Patricia
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Patent No. 6420157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Vet. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERMYURE TROCKMATION: Description of Artificial Sequence: Fusion gene OTHER INFORMATION: with homo sapien serine protease catalytic domain
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527 CAACATCACCATCATTCAACCACCAGAAGTGTGAGAACCCCTACCCCGGCAACATCACAGA 586
607 ACCACGGCCGCCCGGAGAGTGAAGTACAACAAGGGCCTGACCTGCTCCAGCATCACTATC 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       647 GGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCATTATCTCCTGGGGCCCAGGATCCGTG
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                                                                                                                                                                                                                                                                                                             CATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCCCTGGGGTTCCAAAGTGAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 299; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 159.6; DB 4; Length 1049; Pred. No. 6.9e-32;
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Gaps

US-09-0	IN		9	Oy Oy Oy Oy OS-OG- US-OG- Fares	B & B & B & B
TYPE: INCLESS edit:  TYPE: INCLESS edit:  TYPE: INCLESS edit:  TOPOLOGY: linear  IMPEDATE SOURCE:  LIBRARY: COLMOT27  CLONE: 1798496  SEQUENCE DESCRIPTION: SEQ ID No: 19:	NUMBI - AUNI NFORMA - Petel N NUMBI - Petel N NUMBI - Petel N NUMBI - Petel N NUMBI - Petel N NUMBI - Petel N NUMBI - Petel N NEORMA - Petel N NUMBI - Petel N NEORMA - Petel N NUMBI - Petel - NUMBI - NUM	STATE: CA.  GOWNTY: USA  COUNTY: USA  COMPUTER READABLE FORM:  COMPUTER: LOW Compatible  APPLICATION MOMBER: US/09/008,271A  REPLICATION MOMBER: US/09/008,271A	NERAL INFORMATION:  APPLICANT: Hailman, Jennifer L.  Hilman, Jennifer L.  Guegler, Mart J.  Guegler, Mart J.  Guegler, Mart J.  Congress Const. C.  TITLE OF INFERTION, HUMAN PROTEASE MOLECULES  NUMBER OF SEQUENCES: J.  CORRESCONDENCE, ADDRESS:  ADDRESSES: INCYC Pharmacouticals, Inc.  GTR.EFI. 31/4 Porter Dr.  GTR.EFI. 31/4 Porter Dr.	947 CARCITENTENACCACANTICANATACTOCTOGANCANAMATORINGCTRC 906  967 CATGAGGETATACCANCANCINCCTOGACTOGACTOGANCANTANAMATORINGCTAC 946  907 ACCTGAGGETATACCANCANTENCCOCCTACCTOGACTOGANCANGANGANGANGANGCTANGCTACTOGACTOGACTOGANGCTANGCTANGCTANGCTANGCTANGCTANGCTANGC	547 ACTGTCACCAGTCCCCCGAGAGAATTTTCCCTGACACTCTCAACTGTGCAGAGATAAATC 606 667 CTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGGCGTGGCACAACATGAATATGT 726 607 TTCCCCAAAGAAGTGTGAAGGTCTTCTACCTGGCGTGGTCACAACATGAATATGT 726 607 TTCCCCAAAGAAGTGAGAGAGACCTTACCCAGGGGAGAAGATGAACTGTGTGT 666 727 GTGGACTGGAACAGGGGCCAGAACTGTCTGGCAGAGTGAACTCTGAGAGCCCCCTGGTCTGT 786 667 GCAGGCAGCACACACACACACACACACACACACATGTCTTTCGAGAGCCCCCTGGTCTGT 786 667 GCAGGCAGCACACACACACACACACACACACACACACAC

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                                894 AGTCATACGCTCCAACTGAT 913
                                                                                              834 CTCTGCCCAGCATCCAGCTGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAATAA 893
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916 GATCATAGGCAGCAAGGGCT 935
                                                                   856 GAGGTČČGÁCAÁAČČTGGCGŤČŤÁTÁCCAÁCÁŤČŤGČCGCŤÁČCŤGGAČŤGGÁŤČÁÁGÁÁ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 GACGACTCGCTCTGTTGTCCATCCCAAGTACCACCAGGGCTCAGGCCCCATCCTGCCAAG
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RESULT 15

SEQUENCE 1, Application US/09070526

SEQUENCE 1, Application US/09070526

PROBLEM NO. READ STORMER

APPLICANT: CLINKENHEAD HELD

APPLICANT: CLINKENHEAD HELD

APPLICANT: CLINKENHEAD HELD

APPLICANT: DINKESS, USA

ITILS OF INVENTION: NO. 6100059e1 Compounds

NUMBERS OF SEQUENCES: A FRESTIA

COMPERS PROMESSE: DANNER & PRESTIA

COMPERS UNA SPORE

STATE: NO. BOX 980

STATE: 19482

COMPTEX: USA

COMPTEX: USA

ZIP: 19482

COMPTEX: BRADALE PORM:

COMPTEX: PRES: DIABETER STATE: 19482

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US-09-070-526-1
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TELEX: 861659
THEOMETION FOR SEC ID NO. 1
SEQUENCE CHENCERSTICS:
ENGIN: 944 base pairs
TYPE: DINCISC 61614
STRANDEDNESS: single
TOPOLOSI: 11.Tear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.6
Best Local Similarity 53.8
Matches 366; Conservative
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APPLICATION NUMBER: 08 9711952.3

FILING DATE: 9-JUN-1997

APPLICATION NUMBER: EB 9709646.4

FILING DATE: 1-DEC-1997

APTONNEY AGENT INDONATION:

NAME: PRESTIN, PAUL F

REGISTRATION NUMBER: 23 031

FRECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0710

TELEPHONE: 610-407-0710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM COMPACTIBLE
OPERATING NUTRIES
SOPPHARE: Rest-ESD for Windows Version 2.0
CURRENT APPLICATION NATM.
APPLICATION NUMBER: U8/09/070,526
FILING DATE: 30-RP-1998
CLASSITICATION: PRP-1998
CLASSITICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 10.6%; Score 154; DB 3; Length 944; Local Similarity 53.8%; Pred. No. 1.8e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 GROCCOCOCCOCTOCARCOCTROCAROTTCCTCTCARCOCCTCTCTCARCOCCCTTCTCCRCTPC 293
218 GROCCARCCCCATTCCCARCCTTGCCARGCGCTTGTTCCAGGGCCAGCAAYFACTCTG 277
                                                                                 686 TGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGGGATTCTGGAGG 745
                                                                                                                                                                                                                    626 AGAAGTAĀAĀTĊTTTCCĊĊAGĀĀGAĀGTĠTĠĀĠĠATGCTTĀĊĊĊĠĠĠGCĀĠATĊĀĊĀGĀ, 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 GACGACTCGCTGTTGTTCCATCCCAAGTACCACCAGGGCTCAGGCCCCATCCTGCCAAG 473
774 CCCCCTGGTCTGTGACGAGACCCTCCAAGGCATCCTCTCGTGGGGGTGTTTACCCCTGTGG 833
                                                                                                                                                  714 CAACATGATATGTGCTGGACTGGACCGGGGCCAGGACCCTTGCCAGAGTGACTCTGGAGG 773
                                                                                                                                                                                                                                                                                     654 CAGCATCACTATCCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGGCGTGGTCACCAA 713
                                                                                                                                                                                                                                                                                                                                                            566 CTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGTTTTTCCTGACACTCTCAACTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 ACTGTGGGGTGGAGTAGGGGATGATCACCTGCTGCTTCTTCAGGGGGGAGCAGCTCCGCCG 413
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866 GGGCGAAGGCAGCAAGGGCT 885
                                       894 AGTCATACGCTCCAACTGAT 913
                                                                                                      834 CTCTGCCCAGCATCCAGCTGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAATAA 893
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Search completed: November 25, 2003, 07:31:35 Job time : 105 secs

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                                                                                                                                          nucleic search, using sw model
November 25, 2003, 04:52:03 | Search time 425 seconds (vi i Sharch time 425 seconds (provember 25, 2003, 04:52:03 | Search time 425 seconds (provember 25, 254 Million cell updates/sec
                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Scoring table:	Title: US-1 Perfect score: 1454 Sequence: 1 AC
Scoring table: IDENTITY_NUC	US-10-021-368-2 1454 1 ACCMGCGGCAGACCACAGGCGTCGTGAAAAAAAAAAAA

Searched: 2552756 seqs, 1349719017 residues Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database

IN Countered, 1541m013\*\*

1 /SIDSI/gogdata/genesed/geneseqn-embl/MA1980\_DAT\*\*
2 /SIDSI/gogdata/genesed/geneseqn-embl/MA1980\_DAT\*\*
3 /SIDSI/gogdata/genesed/geneseqn-embl/MA1980\_DAT\*\*
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28 /SIDSI/gogdata/genesed/geneseqn-embl/MA1980\_DAT\*\*
29 /SIDSI/gogdata

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Breast cancer rela	ABL63744	24		35.0	508.4	00
Breast cancer rela	ABL63341	24		35.0	508.4	7
Human ovarian anti	ABQ55252	24		43.1	627	6
DNA encoding novel	ABK31771	24	831	57.0	829.4	U
Human gene express	AB234966	24		99.2	1442	4
Human serine prote	ABT06519	24		100.0	1454	w
cDNA encoding huma	ABS76452	24		100.0	1454	N
Human NES1 cDNA.	AAT44111	18		100.0	1454	,
Description	ID	DB 8d	Length DB	Query	Score	Result

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9
165.8	173.8	173.8	173.8	173.8	173.8	203.4	203.4	243.4	256	267.2	267.2	267.2	274.6	295	319	319	329.4	335.6	345.4	352	353	353	367	376	376	376	376	376	379.6	383.8	438.4	445.4	447.4	448.4	508.4	508.4
11.4	12.0		12.0	12.0	12.0	14.0	14.0	16.7	17.6	18.4	18.4	18.4	18.9	20.3		21.9				24.2				25.9					26.1	26.4	30.2	30.6	30.8	30.8	35.0	35.0
1166	1185	1091	1091	1091	1091	319	205	267	274	283	283	283	292	339	321	321	349	377	359	421	373	373	434	396	396	396	396	396	430	399	468	470	449	454	532	532
22	22	22	21	21	21	22	22	24	24	24	24	24	24	24	25	22	24	21	24	24	25	22	24	24	24	24	24	24	24	24	24	24	24	24	24	24
AAD14841	AAH98653	AAF54341	AAA37075	AAA77671	AAC58114	AAH83124	AAS24516	ABL79810	ABL79814	ABL82297	ABL67485	ABL67055	ABL81595	ABL82894	ABZ33597	AAI29411	ABL80212	AAZ80588	ABL82352	ABL81769	ABZ33513	AAI29327	ABL79953	ABL81574	ABL66152	ABL64839	ABL63950	ABN94495	ABL81770	ABL82197	ABL79803	ABL79800	ABL82374	ABL82657	ABL82556	ABL67277
	Human EST-derived	ncoding p	PRO1303	PRO1303	PR01303	ovarian	ovarian	Human ovarian canc	ovarian			id cancer				_	_				-			n ovaria	cancer	Lung cancer relate	Breast cancer rela		ovarian	ovarian	ovarian	ovarian				Thyroid cancer rel

#### ALIGNMENTS

AAT44111 standard; cDNA; 1454 BP.

AAT44111;

28-FEB-1997 (first entry)

Human NES1 cDNA.

NES1; malignancy; cancer; breast carcinoma; cervix carcinoma; prostate carcinoma; gene therapy; diagnosis; prognosis; serine protease; ss.

Homo sapiens.

RESULT 1

ANT44111

TO ANT4

ANT44111

TO ANT4

TO ANTA4

TO ANTAA

TO AN 06-JUN-1995; 21-MAY-1996; 12-DEC-1996. polyA\_signal WO9639175-A1. 95US-0467155. 96WO-US07343 /\*tag= a 1348..1353 /\*tag= b Location/Qualifiers

(NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC

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Matches 1454; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A cDNA clone (AAY4411) retmed NSS1 (for Normal Epithelial Specific-1), codes for a serine protease (AAM07420) negatively associated with spithelial coll malignancy. A radiation-transformed human mammary spithelial cell (NEC) line, 768-30, was established from a normal NEC strain, 76N py gamma-irradiation. Subtractive hybridisation between 76N and 78R-30 gamma-irradiation. Subtractive hybridisation between 76N and 78R-30 cells yielded the NESI clone, whose mRNA expression was greatly decreased in 78R-30 cells. NESI provides a diagnostic marter for breast, cervical and presence carcinomas and can provide genetic constructs for cancer the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide carcinomas and can provide genetic constructs for cancer to the provide genetic constructs for the provide genet
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   TGGGGCACCACGCCCGGAGAGTGAAGTACAACAAGGGCCTGACCTGCTCCAGCATC
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1440 1440	GTCATGTAAGGCTTAACACAGTGGGTGAGTTCTGACTTAACGTTACCTGTTGTTCGT	1381 1381
1380 1380	TCTTAGACATGTTGTGAGGAGACTATGATATATACATGTGTATGTGAATCTTCATGTGATTT	1321
1320 1320	AGTOCCCCTCTTGAACCTCAGTTTCCTCATCTCCGAAAATGGGAACAATGACGTGCCTACC	1261 1261
1260 1260	CTGGGGTCACCCAACCTCACTTCCTCTCCACTCCCCCCTTGTGACTTTTGGCAAGCA	1201
1200	CALAGOTTYATTCCAAGAACCCAGGAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTA	1141
1140 1140	CATTICCCCACCTATCCCCATTCTCTGCTGTACTGAAGTGAAATGCAGAAAGTGGTGA	1081
1080	TOTCH CACHETT CHANCE TOTCH COOCCUTT CACHETT CACHETT COCCUTT CACHETT CA	1021
1020 1020	CARATROCCARAGOCTICCATOGTICCATCTCTTCCTCCCATTGGGTGAACTCTCCCCCT	961 961
960	GETTCCAACTGATCCGAGATGCTACCCTCCACCTGATCCGAGATGTTATCCTCCTGCTGATCCGACTGATCCACCTGATCCACCTGATCCACACTGATCCACACTGATCCACCTGATCCACACTGATCCACACTGATCCACACTGATCCACACTGATCCACACTGATCCACACTGATCCACACTGATCCACACTGATCCACACTGATCCACACTGATCCACACTGATCCACACACTGATCCACACACTGATCCACACTGATCCACACACTGATCCACACACTGATCCACACACTGATCCACACACTGATCCACACACTGATCCACACACTGATCCACACACTGATCCACACACTGATCCACACACTGATCCACACACTGATCACACACA	901
900	CAGCAPTCCAGCTTTCTACACCCAGATCTGCAAATACATGTCCTGGATCAATAAAGTCATA	841
840 840		781 781
780 780	ATATOTOCACTOCACTOCACCCACCACACCTTTCCCACACTTCACACCCCCTG	721 721
720	ACTATOCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGGCGTGGTCACCAACAACATG	661

ABS76452 standard; cDNA; 1454

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ABS76452

(first entry)

CDNA encoding human ovarian cancer marker OV32

Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacerial meningitis; vtral meningitis; hlzneimer's disease; Parkinson's disease; cerebral codema; hydrocephalus; brain hemiation; hiflammation; encephalitis; testicular disorder; nonthervalous granulomatous sorchitis; connective tissue disorder;

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                                                                                                                                                                                                           The present invention relates to a new method for assessing whether a priest is efficied with couring cancer. The mathod involves commanding the expression level of a marker in a patient sample and the normalized the expression of the marker in a patient sample and the normalized of expression of the marker in a control non-ovarian cancer sample where the marker is selected from 363 cancer markers described in the control non-ovarian cancer as early as expectionation. The method of the threation is useful in diagnosing or characteristing cancer, in detecting the presence of cancer as early as expectation of the patients having a samilal history of ovarian cancer. The method may also be particular use with patients having a samilal history of ovarian cancer. The cancer markers may be used in the analogement and treatment cancer. The cancer markers may be used in the analogement cancer that it is a concern to the cancer markers may be used in the analogement cancer. The cancer is a concern to the control of the c
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                               Matches 1454;
                                                                                                                                                                                                        Sequence 1454 BP; 289 A; 481 C; 377 G; 307 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assessing whether a patient is afflicted with ovarian cancer, useful in
assessing the stage or progression of the disease, comprises comparing
the expression level of a cancer marker in a sample from a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monahan
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19-SEP-2001;
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DB; ABG96356.
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Morrisey MP, Olandt PJ, Sen A, Vi
u K, Schmandt RE, Zhao X, Glatt K;
                                                                                                                               Conservative
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100.0%; Pred. No. 0;
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                           The present invention relates to a method of diagnosing a cellular proliferative disorder of breast tissue, which involves determining the state of methylation of one or more nucleic acids isolated from the subject, where the state of methylation of the nucleic acids as compared with a state of methylation from a subject not having the cellular proliferative disorder of breast tissue in the subject. The nucleic acids proliferative disorder of breast tissue in the subject. The nucleic acids may be THIST, MOXAS, NEST, Testings acid receptor beta (RANGER) at Signa, perceptor, cyclin ps. Wilms, tumour gene (WT-1), 43.3 signa, and top makes the subject of the subject of decembining and the subject of the su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biagnosing and/or determining a predisposition to a cellular proliferative disorder of breast tissue, in particular breast cancer, by decermining the state of methylation of one or more nucleic acids
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      predisposition to a cellular proliferative disorder, in particular
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Best Local
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breast cancer including ductal carcinoma in situ, lobular carcinoma, colloid carcinoma, tubular carcinoma, medullary carcinoma, metuplassic carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and oppillary carcinoma in situ. The present sequence is a gone fragment used oppillary carcinoma in situ. in the exemplification of the invention.

Sequence 1454 BP; 289 A; 481 C; 377 G; 307 T; 0 other;

2	1 SEMILITITY 100.0%; Score 1454, DB 24; Length 1454; 1 SEMILITITY 100.0%; Fract No. 0; Indels 0; Gaps 1454, Conservative 0; Mismatches 0; Indels 0; Gaps 1456, Conservative 0; Mismatches
Dy Qy	01 STCCTGGTGGACCAGAGTTGGGTGCTGACGGCCCCGCACTGCGGAAACAAGCACCACTGTGG 111111111111111111111111111111111
B &	61 GCTCCHGTAGGGATGATCACCTGCTGCTTCTTCAGGGCGAGCAGCTGCGCCGGACGACT 
B &	21 COCTCTGTTGTCGATCCCAAGTACGACGACGACGACGATCCAACGCGCAAACGCGAAACGAACG
Db Qy	81 GATGAGGAGGATCTCATGTTGCTAAAGCTGGCCAGGCCCGTAGTGGGGGGGG
B 8	41 CGGGCCCTGCAGCTTCCCTACCGCTGTGCTCAGCCCGGAGACCAGTGCCAGGTTGCTGGC 41 CGGGCCTCCAGCTTCCTACCGCTGTGTTGCTGGC 41 CGGGCCTCGAGACTTCCTACCGCTGTGTAGCCAGAAACCAGTGCAGGTGCTGGC
음 성	601 TOGGGCACCACGGCCCCCGGAGAGTGAAGTACAACAACAACGGCCTGACCTGCTCCACCATC 660
B 8	661 ACTATICCTRAGECCTAAAGAGTGRAGGTCTTCTACCTTGGGGTCACCAACAACTG 720
8 8	721 ATATOTOCTOSACTOSACCOSOCCACGACCCTTOCCASACTACTCTOCAGCCCCCCTC 780
B 8	781 OFFICTARCA ACCOMPCIANCE CONTROL OF THE CONTROL
B 65	841 CACCATCCACCTGTCTACACCCAGATGTGCAAATACATGTCCTGGATCAATAAAGTCATA 900 841 CACCATCACCACCTGTTAAACCCAGATCCAATACATCATAAGTCATA 900
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New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease
                                                                            WPI; 2002-740862/80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; artery; endochelium; umbilical; vein; acrea; pulmonary artery; bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast; tumour; microarray; genome mapping; antibiocto; antivital; antifungal)
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                                                                                                                                                                                                                                                                                             20-MAR-2002; 2002WO-US08456.
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pathologies involving alterations of gene expression, e.g. cancer

Claim 3; Page 273; 850pp; English.

or the invention relates to a gene expression profile comprising one or more consequence of the control of the

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Sequence 1457 BP, 293 A; 480 C; 377 G; 307 T; 0 other;

Score 1442; DB 24; Length 1457;

Query Match

S 밁 밁 Ş Ş 밁 Ş 밁 Ś á S 밁 밁 몆 S B Matches 1453; Match 99.2%; Local Similarity 99.9%; 541 CGGGCCCTGCAGCTTCCCTACCGCTGTGCTCAGCCCAGAGACCAGTGCCAGGTTGCTGGC 600 481 GATGAGCACGATCTCATGTTGCTAAAGCTGGCCAGGCCCCGTAGTGCCGGGGGCCCCGCGTC 361 301 241 181 181 421 421 361 241 121 GCCCGGGCTCTGGCGAAGCTGCTGCCGCTGATGGCGCAACTCTGGGCCGCAGAGGCG 61 13 GATGAGCACGATCTCATGTTGCTAAAGCTGGCCAGGCCCGTAGTGCCGGGGCCCCGCGTC OGCTCTGTTGTCCATCCCAAGTACCACCAGGGCTCAGGCCCCATCCTGCCAAGGCGAACG GCTCGAGTAGGGGATGATCACCTGCTGCTTCTTCAGGGCGAGCAGCTCCGCCGGACGACT CGCGGCTCGCAGCCCTGGCAGGTCTCGCTCTTCAACGGCCTCTCGTTCCACTGCGCGGGT GCGCTGCTCCCCAAAACGACACGCGCTTGGACCCCGAAGCCTATGGCGCCCCGTGCGCG GECGACTCCCAGATCCTGGCCATGAGAGCTCCGCACCTCCACCTCTCCGCCGCCTCTGGC GGCGACTCCCAGATCCTGGCCATGAGAGCTCCGCACCTCCACCTCTCCGCCGCCTCTGGC CGCTCTGTTGTCCATCCCAAGTACCACCAGGGCTCAGGCCCCATCCTGCCAAGGCGAACG GCTCGAGTAGGGGATGATCACCTGCTGCTTCTTCAGGGGGGAGCAGCTCCGCCGGACGACT GTCCTGGTGGACCAGAGTTGGGTGCTGACGGCCGCGCACTGCGGGAAACAAGCCACTGTGG CGCGGCTCGCAGCCCTGGCAGGTCTCGCTCTCAACGGCCTCTCGTTCCACTGCGCGGGT GCGCTGCTCCCCCAAAACGACACGCGCTTGGACCCCGAAGCCTATGGCGCCCCCGTGCGCG GCCCGGGCTCTGGCGAAGCTGCTGCTGCTGATGGCGCAACTCTGGGCCGCAAGAGCG Conservative 0; Mismatches Pred. ŏ. 0; Indels -420 360 300 300 180 120 60

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                                                                                                                                         #GTGCCCTCTCTGAACCTCAGTTTCCTCATCTGCAAAATGGGAACAATGACGTGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GCTCCAACTGATCCAGATGCTAACGCTCCAGCTGATCCAGATGTTATGCTCCTGCTGATC 959
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Of the present invention relates to the isolation of novel human contracts and the multic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as to cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. infilamentory diseases and asthma), cardiovascular diseases and contexts (e.g. intended in the context of the contex
Sequence 831 BP; 146 A; 287 C; 245 G; 153 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Fig 1CC; 313pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding novel human proteases, useful for useful treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-139913/18
P-PSDB; AAU82729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, processe; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; netabolic disorder; inflammatory disorder; neuronal-associated disease; netabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain, mood disorder; bypartension, psychotic disorder; neurological disorder; dyskinesia; utral infection; human immunodeficiency virus; HTV: non-viral infection;
                                                        the novel human proteases of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charydczak
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                                                                                                                                                                                82 ATGAGAGCTCCGCACCTCTCCGCCGCCTCTGGCGCCCCGGGCTCTGGCGAAGCTG
                                                                                                                                                                                                                            Similarity
              GTCTCGCTCTTCAACGGCCTCTCGTTCCACTGCGCGGGTGTCCTCGTTGGACCAGACTTGG
                                                CTGCCGCTGCTGATGGCGCAACTCTGGGCCGCAGAGGCGGCGCGCTGCTCCCCCAAAACGAC
GTCTCGCTCTTCAACGGCCTCTCGTTCCACTGCGCGGGTGTCCTGGTGGACCAGAGTTGG
                                                                   ACGCGCTTGGACCCCGAAGCCTATGGCGCCCCGTGCGGGGCGCGGCTCGCAGCCCTGGCAG
                                                                                                    CTGCCGCTGCTGATGGCGCAACTCTGGGCCGCAGAGGCGGCGCCGCTGCTCCCCAAAACGAC
                                                                                                                                                      ATGAGAGCTCCGCACCTCCACCTCTCGCCGCCTCTGGCGGCCCCGGGCTCTGGCGAAGCTG
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                       57.0%;
                                                                                                                                                                                                                       Score 829.4; DB 24;
Pred. No. 7.9e-179;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                    Length 831;
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                                                                                                                                                                                                           Gaps
240
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standard, DNA; 831

ВP

23-APR-2002 ABK31771

(first entry)

DNA encoding novel human protease

#28

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322

GTGCTGACGGCCGCACTGCGGAAACAAGCCACTGTGGGCTCGAGTAGGGGATGATCAC

381

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Birse CE, Rosen CA;

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                                                                                                                                                                                                                                                                                                                                                        Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; tumour; ovarian cancer; tumour; expedanctive system disorder; infertility; pregnancy disorder; anovulation; polyopitic ovary syndrome; pros, ovarian, oyar; dysmenorthoes; endocrine disorder; ovarian; entitlementory condition; immune disorder; blood disorder; orathovascular disorder; urinary system disorder; dug screening; generation; officers; urinary system disorder; dug screening; generation; orathorapy; disorder; urinary system disorder; urinary system disorder; antioned preparation; orathorapy; disorder; urinary system disorder; urinary system disorder; generation; orathorapy; orathorapy; generation; orathorapy; orathorapy; generation; orathorapy; orathorapy; generation; orathorapy; orathorapy; orathorapy; generation; orathorapy; orathorapy
                                                                                   07-JUN-2000; 2000US-209467P
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                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                       07-JUN-2001, 2001WO-US18569
                                                                                                                                                                                                                                                           WO200200677-A1
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ovarian antigen HCOPE27 cDNA, SEQ ID NO:1132.
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CTCGTGGGGTGTTTACCCCTGTGGCTCTGCCCAGCATCCAGCTGTCTACACCCAGATCTG

869 300 CCCTTGCCAGAGTGACTCTGGAGGCCCCCTGGTCTGACGAGACCCTCCAAGGCATCCT 809 CTTCTACCCTGGCGTGGTCACCAACAACATGATATGTGCTGGACTGGACCGGGGCCAGGA CTTCTACCCTGGCGTGGTCACCAACAACAACATGATATGTGCTGGACTGGACCGGGGCCAGGA 749

CTCGTGGGGTGTTTACCCCTGTGGCTCTGCCCAGCATCCAGCTGTCTACACCCAGATCTG

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GTACAACAAGGGCCTGACCTGCTCCAGCATCACTATCCTGAGCCCTAAAGAGTGTGAGGT 180 GTACAACAAGGGCCTGACCTGCTCCAGCATCACTATCCTGAGCCCTAAAGAGTGTGAGGT TCAGCCCGGAGACCAGTTGCCAGGTTGCTGGCGCACCACGCCCCCCCGGAGAGAGTGAA gechagecongradrecogggecoccederoceggecorrecagerrecoracegrate

689 629 60 Matches 652; Query Match Best Local Similarity

Conservative

510 GGCCAGGCCGTAGTGCCGGGGCCCGGGGCCCTGCAGCTTCCCTACCGCTGTGC

Sequence 750 BP; 144 A; 254 C; 173 G; 169 T; 10 other;

43.1%; Score 627; DB 24; 98.2%; Pred. No. 7.4e-133 0; Mismatches

DB 24; Length Indels

2 Gaps

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The invention relates to 21% noval human overian antigens (ABPA104). Challed the invention and to copie encoding them (ABGSA1134) and also cancepasses polypeptides 90% identical and polymuoleotides 93% identical control the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human overian antigen control of overian antigen polymucleotides against human overian antigens, and the use control of overian antigen polymucleotides and polypeptides in disposing, and the use control of overian antigen polymucleotides and polypeptides in disposit, and the use control of overian antigen polymucleotides and polypeptides in disposit, and the use control of overian antigen polymucleotides and polypeptides in disposit, and the use control of overian property and overian antigen, and the use control of overian property and the use of polypeptides overy syndrome, relatively disposit, and describe the control of overian overian overian antigen polypeptides and control overian property disposit, and toxic shock syndrome, inflammatory conditions (e.g., mastitis, copientis, and toxic shock syndrome, intended property of the property of the polyperty disposit, and copient is, systemic land acquire and toxic shock syndrome, sensor of the polyperty disposit, and toxic shock syndrome, period of the control of the polyperty disposit, and toxic conditions of the polyperty disposit, and toxic control of the polyperty disposit, and the control of the polyperty of the polyperty disposit, and the control of the polyperty of the polyperty
                                             Note: The sequence data for this patent did not form part of the printed specification, but was obstaned in electronic format directly from WIPO at ftp.wipo int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer). Aimmne disorders, cardiovascular disorders and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 1132; 2922pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2002 (first entry)
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2000US-266LI2P
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2000US-276LIP
2000US-277JB
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## (AVAL-) AVALON PHARM.

Soppet Augustus M, Weaver Z; Carter KC, Ebner R, Endress G, Horrigan S

## WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set

# Claim 1; SEQ ID 1678; 44pp; English.

contine present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical cagent to be tested for anti-neoplastic activity, determining a change in copyression of at least one gone (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABLG164 CC to ABL70110), or is at least 531 identical to (S), where a change in a sepression a indicative of anti-neoplastic agent (S) and the sequence (S) and the sequence (S) and the sequence (S) where a change in a sepression a indicative of anti-neoplastic agent and can be used in the sequence which can anti-neoplastic agent, and can be used at the sequence of the sequence of the sequence which can be used in the capital of the sequence o

# Sequence 532 BP; 110 A; 183 C; 113 G; 126 T; 0 other;

Query Match
Best Local Similarity
Matches 531; Conserva 712 ANCARCHIGHTATGCTGGACTGGACCGGGGCCAGGACCCTTGCCAGAGTGACTTGGA 952 180 121 832 772 61 CTGCTGATCCAGATGCCCAGAGGCTCCATCGTCCATCCTCTCCCCCCAGTCGGCTGAA AAAGTCATAGGCTCCAACTGATCCAGATGCTAGGCTCCAGCTGATCCAGATGTTATGCTC GGCTCTG-CCAGCATCCAGCTGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAAT GGCTCTGCCCAGCATCCAGCTGTCTACACCCCAGATCTGCAAATACATGTCCTGGATCAAT GCCCCCTGGTCTGTGACGAGACCCTCCAAGGCATCCTCTCGGGGTGTTTACCCCTGT GGCCCCTGGTCTGTGAGGAGACCCTCCAAGGCATCCTCTCGTGGGGTGTTTACCCCTGT Conservative 35.0%; 0 Score 508.4; DB Pred. No. 6e-106; 0; Mismatches DB 24; Length 532; 1; Indels 2; Gaps 101 951 179 891 120 60 N

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밁 당 밁 밁

28-SEP-2000; 2000US-236034P. 28-SEP-2000; 2000US-23613P. 28-SEP-2000; 2000US-23611P. 29-SEP-2000; 2000US-23611P. 29-SEP-2000; 2000US-23612P. 29-SEP-2000; 2000US-23613P. 20-CEP-2000; 2000US-23613P. 20-CEP-2000; 2000US-23613P.	7-8EP-2000; 2000US-238640P. 27-8EP-2000; 2000US-238681P. 28-8EP-2000; 2000US-236028P, 28-8EP-2000; 2000US-236032P.	2-3EP-2000; 2000US-33563PP. 26-3EP-2000; 2000US-33563BP. 37-3EP-2000; 2000US-32571LP.		22-SBP-2000; 2000US-234599. 22-SBP-2000; 2000US-23459P. 25-SBP-2000; 2000US-2349239. 25-SBP-2000; 2000US-2349239.		05-UN-2000; 2000US-209473P. 05-UN-2000; 2000US-209531P. 18-SEP-2000; 2000US-233133P.	13-DBC-2001.	WO200194629-A2.	Homo sagiens.	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; scomach, lung, prostate; pancreas; carcinoma; antitumour; cancerous; oytostatic; milm's tumour, adenocarcinoma; gene; ds.	Breast cancer related gene sequence SEQ ID NO:2081.	ADD03/44; 15-MAY-2002 (first entry)	RESULT 8 ABL63744 Standard; DNA; 532 BP. XX	480 GASCAGTTACTSGSSTCA-CCAACCTGACTTCCTCTGCCACTCCCTGCTGTGTG 532	-gagcagttactggggtcacccaacctgacttcctctgccactcccccctgtgtg	ANGTEGTEGCAAAGGTTTATTCCAGAGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGA	ADDITIONAL AND CONTRACT AND CON	300 CTCTCCACCTTGTCTCCACTCTTAAACCTCTGCCGCCCCTCCACACCTCTAAACATCTCCC 359	1012 CPCTCCCCTTCCTCACACCTCCAAACCTCTCAAACCTCCCACACCTCCAAACCTCCC 1071	
	OV 952 CTGTTGATCCALATGCCTCALAGGGGTCCACTGCTACCACTGCTACCACTGCTACCACTGCTACCACTGATCACTGATCACACTGATCACTGATCACTGATCACTGATCACTGATCACTGATCACTGATCACTGATCACTACTACACTGATCACACTGATCACACTGATCACACTGATCACACTGATCACACTGATCACACTGATCACACTACACACAC	Oy 832 GGCCTGCCAGGATCAGGCTGTCTACAGCCAGATCTGCAAATACAGAATACAGAATACAGCAGATCAGCAGATCTACAACAGAATCAGCAAAATACAAGAATACAAGAATCAGCAAAATACAAGAATACAAGAATCAGCAAAATACAAGAATACAAATACAAATACAAATACAAATACAAATACAAATACAAATACAAATACAAAATAAAAAA	97 772 GOCCOCOGOTOTOTIAN GRANACOCTOCIAN GOCATOCTOCOTOTO DE LO 11 11 11 11 11 11 11 11 11 11 11 11 11	bb         1 Accharanterrorgress/resources/corescences/cor	Query Match 35.0%; Score 508.4, DB 24; Leng Best Local Similarity 99.4%; Fred. No. Ge-106; Matches 531; Conservative 0; Mismatches 1; Indel	Sequence 5		CC result of mi, and the data is sufficient to convey the CC structure and/or properties of the agent. Mi can be use		cc expression to an according form (17 or a ordinature guidence (C comprises a sequence (S) selected from 847 sequences (C expression is indicative of anti-neoplastic activity. (C expression is indicative of anti-neoplastic activity. (CC activity and can be used in gene therapy, M1 can be use				WPI; 2002-	AA PI Young PB, Augustus M, Carter KC, Ebner R, Endress G PI Soppet DR, Weaver Z;	(AVAL-) AVAI	03-OCT-2000; 03-OCT-2000; 01-NOV-2000;		02-OCT-2000;	00-00-000

Ebner R, Endress G, Horrigan S;

e agent involves exposing cells to a for anti-neoplastic activity, and serion of a gene of a signature gene set

writhes a method (M1) for screening for an method involves expecting ceals to a chemical particle divolves expecting ceals to a chemical particle of the control of the ceal o a and Wilm's tumour.

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                                                                                                                                                                                                                                                                                              ACTGGACCGGGCCAGGACCCTTGCCAGAGTGACTCTGGA 771
                                                                                                                                                                                                                                                                                                                                                     Score 508.4; DB 24; Length 532; Pred. No. 6e-106; Mismatches 1; Indels 2;
                                                                         AGGCTCCATCGTCCATCCTCTTCCTCCCAGTCGGCTGAA 1011
                                                                                                                                                                                             TGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAAT 891
                                                                                                                                                                                                                                   NGGCTCCATCGTCCATCCTCTTCCTCCCCAGTCGGCTGAA 299
                                                                                                                                                                             TGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAAT 179
                                                                                                                                                                                                                                                                                                                                                       2; Gaps
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> 1132 1072

AAGTOGTOGCAAAGGTTATTCCAGAAAAGCCAGGAAGCCCGTCATCACCCAGCCTCTGA 1191 

CTCTCACCTCATTCCCCCACCTATCCCCCATTCTCTGCCTGTACTGAAGCTGAAATGCAGG 113:

AAGTGGTGGCAAAGGTTTATTCCAGAGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGA

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420 360

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RESULT 9
ABL67277
ID ABL6
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20-SEP-2000

20-SEP-2000

21-SEP-2000

22-SEP-2000

22-SEP-2000

23-SEP-2000

25-SEP-2000

26-SEP-2000

27-SEP-2000

28-SEP-2000

29-SEP-2000

20-SEP-2000

20-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2001; 2001WO-US10838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thyroid cancer related gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL67277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL67277 standard; DNA; 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCAGTTACTGGGGTCACCCCAACCTGACTTCCTCTGCCACTCCCCCCCTGTGTG 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGCAGTTACTGGGGTCA-CCAACCTGACTTCCTCTGCCACTCCCTGCTGTGTG
              2000US 2294739.
2000US 2391328.
2000US 2391328.
2000US 2344099.
2000US 2444099.
2000US 2444099.
2000US 244499.
2000US 244499.
2000US 244597.
2000US 245779.
2000US 255709.
2000US 257709.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:5614.
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Query Match 35.0%; Best Local Similarity 99.4%; Matches 531, Conservative

Score 508.4; Pred. No. 6e-1 0; Mismatches ٥,

. 6e-106; 멾 24;

Indels Length

2 Gaps

S 밁 8 븅 S S Ś

1072 1012

360 300

AAGTOGTOGCAAAGGTTTATTCCAGAGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGA 119: CTCTCACCTCATTCCCCCACCTATCCCCCATTCTCTGCCTGTACTGAAGCTGAAATGCAGG CTCTCACCTCATTCCCCCACCTATCCCCCATTCTCTGCCTGTACTGAAGCTGAAATGCAGG crerecerrigrerocaérigiricaaacerergéegecerecaeacereraaacarerece CTCTCCCCTTGTCTGCACTGTTCAAACCTCTGCCGCCCTCCACACCTCTAAACATCTCCC CTGCTGATCCAGATGCCCAGAGGCTCCATCGTCCATCCTCCTCCCCCAGTCGGCTGAA CTGCTGATCCAGATGCCCAGAGGCTCCATCGTCCATCCTTCCCCCAGTCGGCTGAA AAAGTCATACGCTCCAACTGATCCAGATGCTACGCTCCAGCTGATCCAGATGTTATGCTC AAAGTCATACGCTCCAACTGATCCAGATGCTACGCTCCAGCTGATCCAGATGTTATGCTC GCTCTG-CCAGCATCCAGCTGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAAT GGCTCTGCCCAGCATCCAGCTGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAAT GGCCCCTGGTCTGTGACGAGACCCTCCAAGGCATCCTCTCGTGGGGTGTTTACCCCCTGT GGCCCCTGGTCTGTGACGAGACCCTCCAAGGCATCCTCTCGTGGGGTGTTTTACCCCTGT ANCHACHTRAITATGTGTGGACTGGACCGGGGCCAGACCTTGCCAGAGTGACTGTGGA

묽 문 밁 S 밁

2

952 240 180 892 121 832 772 712

101 1073 299

951 179 168 120 831 60

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The present invention describes a method (M1) for exceeding for an attineoplastic agent. The method involves exposing coll. To a change in case the state of the tested for anti-neoplastic activity, determining a change in comprises a sequence (8) sealected from 8447 sequences (given in BALG164 CC to ABL7011), or is at least 93 identical to (8), where a change in expression is indicative of anti-neoplastic activity. (I) has proceed for screening can anti-neoplastic agent, and can be used for screening can anti-neoplastic agent, and can be used for producing a product which the strictly and can be used for producing a product which can the data collected with respect to the arti-neoplastic agent as a settle data collected with respect to the arti-neoplastic agent as a settle of M1, and the data is sufficient to convey the chemical collected with the second of the complex of the complex of the second of the complex of the complex of the second of the complex of the complex
Sequence 532 BP; 110 A; 183 C; 113 G; 126 T; 0 other;
                                                                      carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for anti-neoplastic agent involves exposing calls to a chemical agent to be tested for amti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-2000; 2000US-237604P.
03-OCT-2000; 2000US-237606P.
03-OCT-2000; 2000US-23760BP.
01-NOV-2000; 2000US-244867P.
01-NOV-2000; 2000US-245084P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 5614; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-188264/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Augustus M,
Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carter KC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endress G,
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420

AAGTGGTGGCAAAGGTTTATTCCAGAGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGA

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                                                                                                                                                                            The present invention describes a composition (1) comprising centriers and immunosticulatins and a polypucipide (III) having a cDNA sequence (2) from the 10912 mulcotide sequence silven in Auti7023.

CC ABL87934, (III) secoding (III) having a sequence (82), a T cell.)

CC ABL87934, (III) secoding (III) having a sequence (82), a T cell.)

CC (II) has cytostatic activity, an oligomuclectide (IV) that hybridises (CC (II) has cytostatic activity, an oligomuclectide (IV) that hybridises (CC (II) has prederably serum or ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprise to contacting a biological sample from a patient with (IV), detecting the amount of polymuclectide hybridising to (IV) and comparing the method comprise the amount of polymuclectide hybridising to (IV) is the contacting th
                                                                  Query Match
Best Local Similarity
Matches 531; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 5534; 489pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polymuclectide encoding polypeptide. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-122075/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ovarian cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian cancer related cDNA clone SEQ ID NO:5534.
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                                                                                                                                    Sequence 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Algate
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                                  712
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  ь.
                                  AACAACATGATATGTGCTGGACTGGACCGGGGCCAGGACCCTTGCCAGAGTGACTCTGGA
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  AACAACATGATATGTGCTGGACTGGACCCGGGGCCAGGACCCTTGCCAGAGTGACTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harlocker
                                                                     Conservative
                                                                                                                                    BP; 110 A; 183
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                                                                                  35.0%;
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                                                                  Score 508.4;
Pred. No. 6e-1
0; Mismatches
                                                                     ç
                                                                                                                                    C; 113 G; 126 T; 0 other;
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                                                                                    .4; DB 24;
6e-106;
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                                                                     Indels
                                                                                                  Length
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ABL82657/c
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The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a overian tumour polypeptide encoded by a polymucleotide (III) having a cDNA sequence (II) from the 10912 mulcotide sequences as given in AELT7023 to
                                                                                                                               Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing
                                                                               Claim 1; SEQ ID
                                                                                                                                                                                                    WPI; 2002-122075/16.
                                                                                                                                                                                                                                    Algate PA,
                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000US-207484P
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                                                                                                                                                                                                                                       Harlocker
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                                                                               5635; 489pp; English
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Human; ovarian cancer; ovarian tumour; cytostatic; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           772 GACCACTAGATORISALCARACCATOCARAGCATACTCTCATGAGGATTATTAACCACTAT
                                                                                                                                                                                                                                                                                                                                                                                                      ovarian cancer related cDNA clone
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Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          simple preferably serum or ovarian tissue. The method comprises mount of polymucleotide hybridising to (IV) and comparing the amount of polymucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thready detecting ovarian cancer in the detected preferably by polymucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCD). (I) comprising (III) and/or (III) is useful for stimulating and/or expanding Teells specific for an ovarian tumour protein comprising contacting cells with (III) or (III) (III) is useful in design and preparation of the tumour polypeptides and proteins in tumour cells) and for tollate a full languit general polypeptides and proteins in tumour cells, and to isolate a full languit general comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    population of 
(I) has cytost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MaLMA7934, (III) encoding (III) having a sequence (83), a T coll
population of (III), or antispen presenting colls that express (III).
(II) has cytostatic activity, an oligonucleotide (IV) that hybridises to
(81) can be used for detecting ovarian cancer in a pattent's biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                    1102
                                                                                                                                                                                                                                                                                                         1042
                                                          1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             922 TAGGTTCAGCTCAGATGTTATGTTCTTCTTGTTGTTCTTCTGCTGATGCCGAGTCCCAGAGGCTCCATC 981
450 TAGGTCCAGCTGATCCAGATGTTATGGTCGTGCTGATCCAGATGCCCAGAGGCTCCATC 391
210
                                                                                                                         270
                                                                                                                                                                                                                                              330
                                                                                                                                                                                                                                                                                                                                                                        390
                                                                                                                                                                                                                                                                                                                                                                                                                                   982
                                                                                                                                                                               TCTCTGCCTGTACTGAAGCTGAAATGCAGGAAGTGGTGGCAAAGGTTTATTCCAGAGAAG 116
                                                                                                                                                                                                                                                                                                                                                                                                          GICCATCCTCCTCCCCAGTCGGCTGAACTCTCCCCTTGTCTGCACTGTTCAAACCTC 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454
    CCAGGAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTACTGGGGTCACCCAACCTGACT
                                           CCAGGAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTACTGGGGTCACCCCAACCTGACT 122
                                                                                                                              TCTCTGCCTGTACTGAAGCTGAAAATGCAGGAAGTGGTGGCAAAGGTTTATTCCAGAGAAG
                                                                                                                                                                                                                                                   TGCCGCCCTCCACACCTCTAAACATCTCCCCTCTCACCTCATTCCCCCACCTATCCCCAT
                                                                                                                                                                                                                                                                                                         GTCCATCCTCTCCTCCCCAGTCGGCTGAACTCTCCCCCTTGTCTGCACTGTTCAAACCTC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.8%;
ilarity 99.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 118 A; 88 C; 149 G; 99 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 448.4; DB 24; Length 454; Pred. No. 2.5e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1, Indels
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    151
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Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polypucleotide encoding polypeptide, annibody specific to polypeptide or T cell expressing
                                                                                                                                                                                                                                                                               06-DEC-2001.
                                                                                                                                                             Claim 1; SEQ ID 5352; 489pp; English
                                                                                                                                                                                                            WPI; 2002-122075/16
                                                                                                                                                                                                                         Algate PA,
                                                                                                                                                                                                                                                    26-MAY-2000; 2000US-207484P
                                                                                                                                                                                                                                                                  29-MAY-2001; 2001WO-US17756
                                                                                                                                                                                                                          Harlocker
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The present invention describes a composition (1) comprising carriers and immunostimulants; and a polyprotected (III) having a cDN sequence (28) from the 10912 incleotide sequences a given in ALP7023 to (28) from the 10912 incleotide sequence as given in ALP7023 to (28) from the 10912 incleotide sequence (28), a T cell; (27) for continuous control of (II) or antique presenting cells that express (II). (28) can be used for detecting overlan cancer in a patient's biological sample preferably serum or ovariant tissue. The method comprises (28) can be used for detecting overlan cancer in a patient's biological sample preferably serum or ovariant tissue. The method comprises (28) can be a biological asmple from a patient with (IV), detecting the camount of polymucleotide hybridising to (IV) and comprising the predetermined cutoff value and thereby describing to (IV) is captility of the comprising context of the comprisi

Sequence 449 BP; 93 A, 160 C; 90 G; 106 T; 0 other;

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Best Local S
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                1110
                                                                       1050
                                             301
                                                                                                                              990
                                                                                                                                                                                       930
                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                870
                                                                                                                                                                                                                                                                          810 CTCGTGGGTGTTACCCCTGTGGCTCTGCCCAGCATCCAGCTGTCTACACCCAGATCTG
                                                                                                                                                                                                                                                                                                                                                     750 CCCTTGCCAGAGTGACTCTGGAGGCCCCCTGGTCTGTGACGAGAGCCCTCCAAGGCATCCT 809
                                                                                                                                                                                                                                                                                                                                                                                            448;
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TGTACTGAAGCTGAAATGCAGGAAGTGGTGGTGGCAAAGGTTTATTCCAGAGAAGCCAGGAAG
                                         TCACACCTCTAAACATCTCCCCTTCACCTCATTCCCCCACCTATCCCCCATTCTCTGCC 1100
                                                                                                                    TCTTCCTCCCAGTCGGCTGAACTCTCCCCTTGTCTGCACTGTTCAAACCTCTGCCGCCC 1048
                                                                                                                                                       AGCTGATCCAGATGTTATGCTCCTGCTGATCCAGATGCCCAGAGGCTCCATCGTCCATCC 240
                                                                                                                                                                              AGCTGATCCAGATGTTATGCTCCTGCTGATCCAGATGCCCAGAGGCTCCATCGTCCATCC
                                                                                                                                                                                                                   CAAATACACGTCCTGGATCAATAAAGTCATACGCTCCAACTGATCCAGATGCTACGCTCC 180
                                                                                                                                                                                                                                         CAAATACATGTCCTGGATCAATAAAGTCATACGCTCCAACTGATCCAGATGCTACGCTCC 929
                                                                                                                                                                                                                                                                                                                                     CCCTTGCCAGAGTGACTCTGGAGGCCCCCCTGGTCTGTGACGAGACCCTCCAAGGCATCCT
                                                                                                    TCTTCCTCCCCAGTCGGCTGAACTCTCCCCTTGTCTGCACTGTTCAAACCTCTGCCGCCC 300
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        30.8%;
                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                          Score 447.4; DB 2
Pred. No. 4.2e-92;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24; Length
                                                                                                                                                                                                                                                                                                                                                                                            1,
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                                                                                                                                                                                                                                                                                                                                                                                                                          449;
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                116
                                                                                                                                                                                       989
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ABLR2374
ID ABLR
XX ABLR
XX ABLR
XX ABLR
XX ABLR
XX Hum
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Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss. Human ovarian cancer related cDNA clone SEQ ID NO:5352.

WO200192581-A2

Homo sapiens

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ACTATGATATAACATGTGTATGTAAATCTT ACTATGATATAACATGTGTATGTAAATCTT 1371

1342

1282

TTTCCTCATCTGCAAAATGGGAACAATGACGTGCCTACCTCTTAGACATGTTGTGAGGAG 134 TCCTCTGCCACTCCTGCTGTGTGACTTTGGGCAAGCCAAGTGCCCTCTCTGAACCTCAG TCCTCTGCCACTCCCCGCTGTGTGACTTTGGGCAAGCCAAGTGCCCTCTCTGAACCTAG 1281

91

90 30

150

1222

RESULT 12

ABL82374 standard; cDNA; 449

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                                                                             Query Match
Best Local Simi
Matches 468;
                                                                                                                                                                                           The present invention describes a composition (1) comprising: carriers and amministerimiants and a polypuchecia (111) has a overlain tumer (2 polypepside encoded by a polypuchecia (111) has a overlain tumer (2 polypepside encoded by a polypuchecia (111) has a overlain tumer (2 polypepside encoded by a polypuchecia (111) has a overlain tumer (2 polypepside encoded by a polypuchecia (111) has a present (11) or overlain cancer (11) overlain cancer (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polymededide encoding polypeptide, antibody specific to polypeptide or T cell expressing
                                                                                                                                                        Sequence 470 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 2778; 489pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI, 2002-122075/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ovarian cancer related cDNA clone SEQ ID NO:2778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL79800 standard; cDNA; 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                  Local Similarity
           470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
  GCTCCATCGTCCATCCTCTTCCTCCCCAGTCGGCTGAACTCTCCCCTTGTCTGACTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGGTCATCACCCAGCCTCTGAGAGCAGT 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTACTGAAGCTGAAATGCAGGAAGTGGTGGCAAAGGTTTATTCCAGAGAAGCCAGGAAG 420
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                                                                                Conservative
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                                                                                                                                                   127 A; 96 C; 142 G; 105 T; 0 other;
                                                                                               30.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones R;
                                                                             0
                                                                             Pred. No. 1.2e
), Mismatches
                                                                                                                   Score 445.4;
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                                                                     . 1.2e-91;
1,
                                                                                                             DB 24;
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                                                                                                             Length 470;
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ABL79803/c
ID ABL79803 :
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The present invention describes a composition (I) comprising; carriers and immunostimulants; and a polypoptide (II) of a ovariant tumour polypoptide encoded by a polymorlocotide (III) having a cpun ce (S1) From the 10912 muclocide sequences as given in ABL77022 to ABL87939, (III) encoding (II) having a sequence (S2), a T cell population of (II) or antigen presenting cells that express (III) consistency of the property of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 2781; 489pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for therapy and diagnosis of ovarian cancer comprising polypoptide of a ovarian numor polypoptide, polymorlectide encoding polypoptide, antibody specific to polypoptide or T cell expressing polypoptide.
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Matches 450
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                       29-MAY-2001; 2001WO-US17756
                                                               06-DEC-2001.
                                                                                                       WO200192581-A2
                                                                                                                                               Homo sapiens
                                                                                                                                                                                       Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss
                                                                                                                                                                                                                            Human ovarian cancer related cDNA clone SEQ ID NO:5175
                                                                                                                                                                                                                                                                    17-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                ABL82197;
                                                                                                                                                                                                                                                                                                                                                        ABL82197 standard; cDNA; 399 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 468 BP; 118 A; 92 C; 152 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1342 ACTATGATATAACATGTGTATGTAAATCTTCA 1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               982 GTCCATCCTCTCCCCCAGTCGGCTGAACTCTCCCCTTGTCTGCACTGTTCAAACCTC 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            922 TACGCTCCAGCTGATCCAGATGTTATGCTCCTGCTGATCCAGATGCCCAGAGGGTTCCATC 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCGCCTCCACACCTCTAAACATCTCCCCTCTCACCTCATTCCCCCACCTATCCCCAT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACGCTCCAGCTGATCCAGATGTTATGCTCCTGCTGATCCAGATGCCCAGAGGCTCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTCCTCATCTGCAAAATGGGAACAATGACGTGCCTACCTCTTAGACATGTTGTGAGGAG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTCCTCATCTGCAAAATGGGAACAATGACGTGCCTACCTCTTAGACATGTTGTGAGGAG 1341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.2%; Score 438.4; DB 24; Length 468; 99.6%; Pred. No. 4.7e-90; tive 0; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 399 BP; 106 A; 86 C; 110 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a composition (I) comprising: carriers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1, SEQ ID 5175; 489pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                         1405 GIGGIGAGIICIGACIAAAGGIIACCIGIIGICGIGAAA 1443
                                                                                                                                                                            1346 TGATATAACATGTGTATGTAAATCTTCAT-GTGATTGTCATGTAAGGCTTAACACAGTGG 1404
                                                                                                                                                                                                                                                                                1286 CTCATCTGCAAAATGGGAACAATGACGTGCCTACCTCTTAGACATGTTGTGAGGAGAGACTA 1349
                                                                                                                                                                                                                                                                                                                                                                                                                 1226 CTGCCACTCCCCGCTGTGTGACTTTGGGCAAGCCAAGTGCCCTCTCTGAACCTCAGTTTC 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1166 GAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTACTGGGGTCACCCAACCTGACTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1046 GCCCTCCACACCTCTAAACATCTCCCCTCTCACCTCATTCCCCCACCTATCCCCCATTCTC 1105
                                                                                                                                                                                                                                                                                                                                                        219 CTGCCACTCCCTGTGTGACTTTGGGCAAGCCAAGTGCCCTCTCTGAACCTCAGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39
                                                                                                                  TGATATAACATGTGTAAATCTTCATGGTGATTGTCATGTAAGGCTTAACACAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.4%; Score 383.8; DB 24; Length 399; 99.2%; Pred. No. 1.1e-77;
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Job time : 430 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenEmbl:*
1: gb_ba:*
2: gb_htg:
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Gapop 10.0 , Gapext 1.0
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1454
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(without alignments)
10930:282 Million cell updates/sec
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gb_ph.
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Copyright (c) 1993 - 2003 Compugen Ltd.
en_bit:
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Unclassified.
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                                   1454 bp
Sequence 2 from patent US 5843694,
AR062140
AR062140.1 GI:5989831
                                                                                                                            AAAAAAAAAAAAA 1454
                                                                                                                                                   GTCATGTMAGGCTTMACACAGTGGGGGGGGTGATGTCTGACTMAGGGTTMCCTGTTGTGGGGG 1440
                                                                                                                                                                                        AGTGCCCTCTCTGAACCTCAGTTTCCTCATCTGCAAAATGGGGAACAATGACGTGCCTACC
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REFERENCE AUTHORS TITLE BASE COUNT ORIGIN FEATURES Query Match Best Local Similarity Matches 1454; Conserv JOURNAL source 121 121 61 61 Methods for identification of modulatory compounds for expression of the MREA protects modulatory compounds for Patent: US 5843694-A 2 01-DEC-1998;
Location/Qualifiers
1.12.1449
/\*regnism="unknown"
289 & 481. 0 377 g 307 t Band, V. GCCGGGCTCTGGCGAAGCTCCTGCCGCTGCTGATGGCGCAACTCTGGGCCGCAAGGCG 180 GGCGACTCCCAGATCCTGGCCATGAGAGCTCCGCACCTCCACCTCTCCGCCGCCTCTGGC 120 GGCGACTCCCAGATCCTGGCCATGAGAGCTCCGCCACCTCTCCACCTCTCCGCCGCCTCTCGC 120 69 THE CONTROLL OF THE PROPERTY OF THE PROPERT (bases 1 to 1454) 100.0%; Score 1454; DB 6; ilarity 100.0%; Pred. No. 1.5e-292; Conservative 0; Mismatches 0; Indels Length 1454; ° 0

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Db 421 CG	1201 CTGGGGTCACCCGACCTGACTTCCTCTGCCACTCCCCCGCTGTGTGACTTTGGGCAAGCCA 1260	망
Qy 421 QG	1201 CTGGGGTCACCCAACCTGACTTCCTCTGCCACTCCCCGCTGTGTGACTTTGGGCAAGCCA 1260	Ş
Db 361 GC	1141 CARAGGTTTATTCCAGAGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTA 1200	₽
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301	1081 CATTCCCCCACCTATCCCCATTCTCTGCCTGTACTGAAGCTGAAATGCAGGAAGTGGTGG 1140	Q
Oy 241 CG	1921 TOTCTSCACTGTTCAAACCTCTSCACGCCCTCCACACCTTAAACATCTCCCCTCTCACCT 1080	당 성
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Db 121 GC	901 CGCTCCAACTGATCCAGATGCTACCCCCCAGATGTTATGCTCCTGCTGATC 960	Db .
. 61	841 CAGCTECARACTICATACACCUAGATICTICARAATTACARGTECCTGGATCAATAAAGTCATA 900 901 CGCTECARCTIGATCCAGATGCTRACGTTCAGGTTGATCCTAGATCATTATACATCCTTCATGATGATACA	9 5
Qy 61 GG	841 CAGCATCCAGCTGTGTACACCCAGATCTGCAAATACATGTGCTGGATCAATAAAGTCATA 900	. 8
Db 1 AC	781 GTCTGTGACGAGACCCTCCAAGGCATCCTCTCGTGGGGTGTTTACCCCTGTGGCTCTGCC 840	Db
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TITLE NES-	601 TGGGGCACCACGCCCGGAGAGTGAAGTACAACAAGGGCCTGACCTGACCTGCACCATC 660	8 8
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SOURCE Unkn	541 COGGCCCTGCAGCTTCCCTACCGCTGTGCTCAGCCCGGAGACCAGTGCCAGGTTGCTGGC 600	Ş
VERSION ARII	481 GATGAGGACGGTTGCTAAAGCTGGCCAGGCCGGTAGTGCGGGGGCCCCGCGTC 540	당 5
DEFINITION Sequ	OTEN CONTROL C	9
	421 GGCTCTGTTGTCCATCGCAAGTACCACCAGGGCTCAGGGCCGCATCCTGCCAAGGCGAAGG 480	B 5
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CGCTCTGTTGTCCATCCCAAGTACCACCAGGGCTCAGGCCCCATCCTGCCAAGGCGAACG
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Puence 2 from patent US 6153387.
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                                                     TICGAGTAGGGGATGATCACCTGCTGCTTCTTCAGGGGGAGGAGCAGCTCCGCCGGACGACT 420
                                                                                                           TCCTGGTGGACCAGAGTTGGGTGCTGACGGCGGCGGCGACTGCGGAAACAACCACTGTGG 360
TCCTGGTGGACCAGAACAAGCTCGTGGGGAAACAAACCACTGTGG 360
TCCTGGTGGAACCAAGCCACTGTGGGAAACAAACCACTGTGG 360
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ent: US 6153387-A 2 28-NOV-2000;
Location/Qualifiers
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AF024605 1454 bp mRNA linear PRI 19-OCT-2000 Homo sapiens scrinc protease-like protease (nest) mRNA, complete	RESULT 4 AF024605 LOCUS DEFINITION H	AFO; LOCI
- AAAAAAAAAAA 1454	1441	рb
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GTCATGTAAGGCTTAACACAGTGGGTGGTGAGTTCTGACTAAAGGTTACCTGTTGTCGTG 1440	1381	D
GTCATGTAAGGCTTAACACAGTGGGTGGTGAGTTCTGACTAAAGGTTACCTGTTGTCGTG 1440	1381	Ş
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AGTGCCCTCTCTGAACCTCAGTTTCCTCATCTGCAAAATGGGGAACAATGACGTGCCTACC 1320	1261	ф
AGIGCCCTCTCTGAACCTCAGTTTCCTCATCTGCAAAATGGGAACAATGACGTGCCTACC 1320	1261	Ş
CTGGGGTCACCCAACCTGACTTCCTCTGCCACTCCCCGCTGTGTGACTTTGGGCAAGCCA 1260	1201	Db
CTGGGGTCACCCAACCTGACTTCCTCTGCCACTCCCCGCTGTGTGACTTTGGGCAAGCCA 1260	1201	Ş
CAAAGGTTTATTCCAGAGAAGCCAGGAAGAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTA 1200	1143	ДD
CAAAGGTTTATTCCAGAGAAGCCAGGAAGCCGGTCATCACCCAGCCTCTGAGAGCAGTTA 1200	114)	Ş
CATTCCCCCACTATCCCCATTCTCTGCCTGTACTGAAGCTGAAATGCAGGAAGTGGTGG 1140	1081	D D
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TWICTSCACTSIT CAAACCTCTGCGCCCCCCCACACCTCTAAACATCTCCCCCTCTAACCT 1080	1023	οg
TGTCTGCACTGTTCAAACCTCTGCCGCCCTCCAACACCTCTAAACATCTCCCCCTCTCACCT 1080	1021	Ş
CAGATGCCCAGAGGCTCCATCGTCCATCCTCCCCAGTCGGCTGAACTCTCCCCT 1020	961	망
. CAGATGCCCAGAGGCTCCATCGTCCATCCTCTCCCCCAGTCGGCTGAACTCTCCCCT 1020	961	Ş
. CGCTCCAACTGATCCAGATGCTACGCTCCAGCTGATCCAGATGTTATGCTCCTGCTGATC 960	901	рь
GGCTGCAACTGATGCAGATGCTAGGCTGAGCTGATGCAGATGTTATGCTCCTGCTGATC 960	901	Q
CAGCATCCAGCTGTCTACACCCAGATCTGCAAATACATGTCCTGGATCAATAAAGTCATA 900	841	В
CAGCATCCAGCTGTCTACACCCCAGATCTGCAAATACATGTCCTGGATCAATAAAGTCATA 900	841	ફ
GTCTGTGACGAGACCCTCCAAGGCATCCTCTCGTGGGGTGTTTAACCCCTGTGGCTCTGCC 840	781	B
GICTSTGACGAGACCCTCCAAGGCATCCTCTCGTGGGTGTTTACCCCTGTGGCTCTGCC 840	781	Ş
. ATATGTGCTGGACTGGACCGGGGCCAGGACCCTTGCCAGAGTGACTCTGGAGGCCCCCTG 780	721	D
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ACTATECTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGGCGTGGTCACCAACAACATG 720	661	9
ACTATCCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGGCGTGGTCACCAACAACATG 720	661	Ş
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TGGGGCACCACGGCCGCCGGGAGAGTGAAGTACAACAAGGGCCTGACCTGCTGCTCCAGCATC 660	603	Ş
CGGGCCCTGCAGCTTCCCTACCGCTGTGCTCAGCCCGGAGACCAGTGCCAGGTTGCTGGC 600	541	Dβ
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GATGAGCACGATCTCATGTTGCTAAAGCTGGCCAGGCCCGTAGTGCCGGGGGCCCCGCGTC 540	481	당
GATGAGCACGATCTCATGTTGCTAAAGCTGGCCAGGCCCGTAGTGCCCGGGGCCCCCGCGTC 540	481	Ş

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301 GTCCTGGTGGACCAGAGTTGGGTGCTGACGGCCGCGCACTGCGGAAACAAGCCACTGTGG
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On Oct 19, 2000 this sequence version replaced gi:1835924.
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Liu, Kazer, D.E., Watanabe, K. and Band, V.
Identification of a novel scrime protease-like gene, the expression
of which is down-regulated during breast cancer progression
cancer kes. 5s (14), 3371-3373 (1996)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: nisc-mgdemjpfr.nih.gov/
Contact: nisc-mgdemjpfr.nih.gov
Bhevdento: N. Wethely, K.D., Becdseron-Sternberg, S.M.,
Benjamin, B. Baldesley, K.D., Bouffard, G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Quan, X., Gupsa, J., Ho, S.-L., Kallin, S., Legaspi, R.,
Lim, W., Naduro, Q.L., Wasiello, C., Mastrian, S.D., McCloakey, J. C.,
Lim, W., Naduro, Q.L., Wasiello, C., Mastrian, S.D., McCloakey, J. C.,
Hobowell, J., Pastron, R., Snyder, B., Sannatripp, S., Thomas, P. J.,
Pandgaon, B. S., Dechman, J. W., Tautgeon, C., Vogt, J.L., Walker, M.A.,
Pandgaon, B. S., Dechman, J. W., Tautgeon, C., Vogt, J.L., Walker, M.A.,
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Tisane Prourement: AFCE
CNBA Library Preparation: Rubin Laboratory
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Sequencing Contest (183C).
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Contact: MGC help desk
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Sudarsanam, S., 03-JAN-2002; Manning, G., Caenepeel, S.

/organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" 287 c 245 g 15 153 rt Length 831;

301 382 CTGCCGCTGCTTGATGGGCGAACTCTGGGCCGCAGAGGGGGCGCTGCTCCCCCAAAACGAC GTCTGCTCTTCAACGGCTCTCGTTCCACTGCGGGGGTGTCCTGGTGGACCAACAAGTTGG ATGAGAGCTCCGCACCTCCACCTCCTCCGCCCCTCTGGCGCGCCCGGGCTCTGGCGAAGCTG ATGAGAGCTCCGCACCTCTCCGCCGCCCTCTGGCGCCCCGGGCTCTGGCGAAGCTG Score 829.4; DB 6; Pred. No. 2.1e-162; 0; Mismatches 1; Indels ç, Gaps 441 321 180 261 120 201 60 360 300 381 240

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FEATURES	TITLE JOURNAL COMMENT	JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS TITLE	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	ACCESSION ACCESSION			5 & B	2 & B	8 8 8	Q Q	
(CTC-51882) overlaps BAC B085745 (CTB-147022, ACO1183) on the left from bases 1 to 2,286 of this accession, and overlaps BAC B0859295 (CTB-318778, AC061977) on the right from bases 120,922 to 122,323 of this accession, Additional chromosome 19 map and sequence information are available at. http://www-bio.lnll.gvo/barp/genome/genome.html.	Direct Submission Submitted (12-007-2000) DOE Joint Genome Institute, Lawrence Livermore Netional Laboratory, Livermore, CA 94550 On Oct 12, 2000 this sequence version replaced gi:7458725. Map and sequence oriented from centromere to g-relonare. BGJ49142		Amico-Keller, G., Coefield, J., Duarre, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kromillar, B., Arellano, A., Sanders, C., Or, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Seguence analysis of chromosome 19q13.4 Unjublished Unjublished C 1039323) DOB Coint Genome Institute. Direct Submission		æ		1416 TGACTRAAGGTTACCTGTTGTCGTGA 1411 5449 TGACTRAAGGTTACCTGTTGTCGTGA 5474	TOTOTATGTAAATCTTCATGTGATGTCATGTAAGCCTTAACACAGTGGGTGG	S269 COGCTETETRACTTTROGCHAGCCHAGTCCACTCTENACCTCACTTCCTCATCTCCCATCTCCA 5228 1296 HANTGGGHACHATGACGTGCCTTACACCTTTGTGACGAGACTATGATXTAACA 1355	ATCACCAGCTCTGAGAGCAAGTTACTGGGGTCTCTGACCCAACCTGATTTCCTCTTCTGCACTCCCCGCTGTGTGACTTTTCTGTCATCATCTGCACCCAGTTTTTGTGATCTGATCTGACCCAGTTTTCTGATCTGACCCAGTTTTGTGATCTGATCTGACCTATCTGACCTGATTTGTGATCTGACCAGTTTTGTGATCTGACCAGTTTTGTGATCTGACTATCTGACCAGTTTTGTGATCTGACCAGTTTGTGACCAGTTTTGTGACCAGTTTGTGACCAGTTTGTGACCAGTTTGTGACCAGTTTGTGACAGTTACTGACAGTTGACAGAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGTTGACAGAAGTGAAGTAGAAGTGAAGTAGAAGTGAAGTAGAAGTGAAGTAGAAGTGAAGAA	1116 CANACITRAANTICOAGANACTOGTIGGCANAGGITTATTICCHGRANAGCCAGGAAGCCGGTC 1175 5149 GAACITRAANTICAAGAAGTAGTATATTICCHGAGAAGCCAGTAGCCGTC 5208 1176 ATCACCCAGCCTCTBAGAGCAGTTACTGCAGGTCACCCCAACTTCCTCTCCACTTC 1235	5029 TOCCOAGTOGGCTGAAACTCTCCCCTTGACCTGCCACTTCAAACCTCTCCACCACCCCCCCC	
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complement(12391, .12498)
/rpt_family="MIR"
12503. 1220
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5878. .6014
/rpt_family="AluSg"
6015. .6043
   / / codon start-1.
// produc-- *rallkrein 10*
// produc-- *rallkrein 10*
// protein id=- hAG23256 1*
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12993 . .1
/rpt fami
13287 . .1
                                                                                                                                                          complement (join(14881. .15033,15498. .15631,15963.
17191. .17371,19124. .19211))
/genew YLKIO,
/notem protease, serine-like, 1"
                                                                                                                                                                                                                                                             /standard_name="stSG30247"
/note="RH48452, WILE-3662-STS"
complement (14432. 14604)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tortes "Rallikrein 10; synonyms; NBS1, PRSS111"
complement (join (14581 . 1503) 151498: 15531,15963. .16237,
17191 . ...1237,19124. .19220,19768. .1979)}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="L2"
complement(13507. .13804)
/rpt_family="AluSq"
complement(14351. .19779)
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complement(12694. .12976)
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complement(11989. .12069)
/rpt_family="MIR"
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complement(11133...11411)
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6422. .6520
                                                                                                                                                                                                                                                                                                                                                                                            product="KLK10 mRNA"
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5037 CCARACTENCTICREAGECCCCTGGTCTGTACGARGCCTCCAAGGCATCCTCTCGTG 14976
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CTGACTAAAGGTTACCTGTTGTCGTGA 1441
                                                                                                                          AAATGGGAACAATGACGTGCCTACCTCTTAGACATGTTGTGAGGAGACTATGATATAACA 14438
                                                                                                                                                                                                                                                            ATCACCAGCTTCTGAGAGCAGTTACTGGGGTCACCCAACCTGACTTCCTCTGCCACTCC
                                                                                                                                                                                                                                                                                                                              GAACCTCAAATCCACGAACTCGTCGCAAACCTTTATTCCAGAGAACCCAGGAAGCCGGTC
                                                           TGTGTATGTAAATCTTCAT-GTGATTGTCATGTAAGGCTTAACACAGTGGGTGGTGAGTT 1414
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complement(16473. .16818)
/rpt_family="812139"
17187. .17912
/rpt_family="81UJO"
17913. .17932
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/rpt_family="(TTGGGG)n"
15715. .15967
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AF243527 230000 bp DNA linear PRI 21-NC Homo sapiens serine protease gene cluster, complete sequence. AF245527

PRI 21-NOV-2000

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REFERENCE
AUTHORS
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Direct Submission
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Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region
Gene 257 (1), 119-130 (2001)
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Paguirigan, C., Pearson, R., Portnoy, M., Reddix-Dupus, M., Schandter, K., Schaller, K., Reddix-Dupus, M., Schandter, K., Schaller, R., Reddix-Dupus, M., Schandter, M., Reddix-Dupus, M., Schandter, M., Miscoccan, R., S.D., Green, R.D., Direct Submission 2002) MIH Intramura: Submisted (14-AUG-2002) MIH Intramura: Submisted (12-WOV-2002) MIH Intramura: Submisted (12-WOV-2002) MIH Intramura: Growmens Citzle, Gaithersburg, MD 30 On Nov 22, 2002 this sequence version Contest Submisted (12-WOV-2002) MIH Intramura: Growmens Citzle, Gaithersburg, MD 30 On Nov 22, 2002 this sequence version Contest Submisted (18-WOV-2002) MIH Intramura: Wab site in Highly Mew. nisc nith-gov Contest odds: NiSG	AC130782 Oxyres clone CH2S1-355A20, W Fan troglodytes clone CH2S1-355A20, W Fan troglodytes clone CH2S1-355A20, W Fan troglodytes (Chippanzee) Fan troglodytes (C	ANAGOSANCANTOACOGCINCCTTCTRABCAT	APPACOAGETTTSAAAGCATTACTGGGTCACC	CHICTURANCA TOTOCCCTOTACCTCATTCCCCCAC  CITTURANCA TOTOCCCTOTACCTCATTCCCCCTCTACCCCCTCTATCCCCCTCTATCCCCCTCTACCCCCTCTACCCCCTCTACCCCCTCTACCCCCTCTACCCCCTCTACCCCCTCTACCCCCACACCTTACCTTACCTTACCTTACCTCTACACCTCACACCTCTACACCTCTACACCTCACACCTCACACCTCACACCTCACACCTCACACCTCACACCTCACACCTCACACCTCACACCTCACACCTCACACCAC	
Picele Pi	Target Pic 88	<u>k-k</u> <u>k-k</u>	3-3 3-3	8-8 8-8	7=

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saley, R.W., Beckerrom-Sternberg, S.M., Boristand, G.G., Brinkley, C., Brooks, S., and B., Bagle, J., Granite, S., Guan, X., Gupta, J., J., Hansen, M., Ho, S.-t., J., Gold, J.W., Karlins, B., S., G., Legaspi, R., Maduro, Q.L., Maduro, V.B., Sasiallo, C., Masteri, B., McDoreall, J., Schandlar, K., Schendlar, M.G., Sison, C., Schandlar, K., Schender, M.G., Sison, C., Brons, P.J., Touchman, J.M., Vogt, J.L., 2921bs, L. Young, A. and Green, E.D.
                                                                                                                                                                                     002) NIH Intramural Sequencing Center, 8717 sithersburg, MD 20877, USA 12)
                                                           002) NIH Intramural Sequencing Center, 8717 ithersburg, MD 20877, USA . sequence version replaced gi:22218452. e Center
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1e CH251-355A20, WORKING DRAFT SEQUENCE, 12
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                                          ramural Sequencing Center
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PEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence it currently consists of 12 contists daps between the contest is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced the accession number will be preserved.

By the finished sequence as soon as it is available and the accession number will be preserved.

28300: contig of 28106 by in length 28300: contig of 1816 by in length 28106: contig of 31566 by in length 28106: contig of 31566 by in length 2822: contig of 31566 by in length 2822: contig of 31566 by in length 2822: contig of 31566 by in length
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Center project name: dhz
Center clone name: 355A20
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                                                                                                                                                               clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                     /organism="Pan troglodytes"
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/clone="CH251-355A20"
/note="assembly_fragment"
                                                                                                                                                                                      note="assembly_fragment
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199463: gap of unknown length
200792: contig of 1329 bp in length
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# contig of 14719 bp in length

# contig of unknown length

# contig of 11584 bp in length

# contig of 6662 bp in length

# contig of 6662 bp in length

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f unknown length
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unknown length
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misc_feature 7322. 33567   Fragment*   misc_feature 12572. 115879   Fragment*   misc_feature 12572. 315879   Fragment*   misc_featu	OY 1356 TOTORNOTAMICTICAL GROWNOSCATORNOCCIDADOCCOGROGOSTOGOSTOGOSTOGOSTOGOSTOGOSTOGOSTOG
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feature 7162: "assembly_fragment" Note="assembly_fragment" Note="assembly_fragment" Note="assembly_fragment" Note="assembly_fragment" Note="assembly_fragment" Note="assembly_fragment" Note="assembly_fragment" Note="assembly_fragment" Note="assembly_fragment" 13900 % 1718 % 1923 fragment" 14909 % 1803 fragment" 14909 % 1803 fragment" 14909 % 1803 fragment" 19464, 200792 feature 19464, 200792 fe	756 133927
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feature	vector side:right" 49975 a 49805 c 48502 g 51409 t
feature 7233. 38567. feature 7233. 38567. feature 8368. 88817. feature 8368. 88817. fragment feature 8368. 88817. fragment feature 8318. 13561. fragment feature 12721. 15597. fragment feature 12721. 15597. fragment feature 12938. 17561. feature 12938. 17562. feature 12938. 17562. feature 12938. 17562. feature 12688. 88817. fragment feature 12688. 88817. fragment feature 12688. 88938. fragment feature 12688. 88938. fragment feature 12688. 89938. fragment	feature 199464200792 /note="assembly_fragment
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_feature 7362383567	_feature 83668. 88817
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-FEB-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
1 (bases 1 to 178504)
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AC140096
AC140096.3 GI:29725783
HTG; HTGS PHASE1; HTGS DRAFT.
Pan troglodytes (chimpanzee)
                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gap between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Hsg Dye; 100 of reads
Chemistry: Dye-terminator Hsg Dye; 100 of reads
Assembly program: phrap; version 0, 99019
Consensus quality: 174918 bases at least Q40
Consensus quality: 17691 bases at least Q20
Consensus quality: 176911 bases at least Q20
Insert size: 159009, agarose-fp
Quality coverage: 15904 sum-of-contigs
Quality coverage: 13.48x in Q20 bases; sum-of-contigs
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2383: contig of 2383 bp in length
2483: gap of unknown length
6759: contig of 4276 bp in length
6859: gap of unknown length
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1115		문양
1055	996 PICCCCAGTICGGCTGAACTCTCCCCTTGTCCTGCACTGTTCAAACCTCTGCGGCCCTCCACA	음 성
995	936 TCCSARTGTTRATGTCCTGCTTGATCCAGATGCCCAAAGGCTCCATCGTCCATCCTCTTCC 108255 TCCSARTGTTRAGGCTCCTGGTCATCATCGCTCTTCCCATCGTCATCATCCTCTTCCATCGTCATCATCCTCTTCCATCGTCATCATCCTCTTCCATCGTCATCATCATCCTCTTCTCATCGTCATCATCATCTCTTTCCATCGTCTTCATCATCTCTTTCTCATCGTCATCATCATCTCTTTCTCATCGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	유 성
935	876 CATGROTGSATCAARTSAAGCCORPACCCCCAACTGARCCAGARGCTACAGCTCAACTGA 108315 CATGROCTGGATCAARTAAAGTCARACCTCCAACTGAATCGAACTGAACT	B 8
875 108	816 GOGGETTANCCCCTOTOGCCCACCACTCCCACCTGCCAACTCCCAAATA 108378 GOGGETTANCCCCTGTGGCCCCCCAGCACTCGCCAACTA 108378 GOGGETTANCCCCTGTGGCCCCCAGCACCCGACCTGTCTANCACCCAACTCTGCCAAATA	B 5
815 1083	755 CCABARTACTITISBAGCCCCCTGSTCTTGTACGBGACCCTCCCAAGGAACTCTCTCTGTGTTGTACGBGACCCTCCCAAGGAACTCTCTCTTGTGTACGBACAACCCTCCCAAGGACACCCTCTCTGTGTACGBACAACCCTGCAAGGAACCCTCTCTGTGTACGBAGACCCTGCAAGGAACCCTCTCTGTGTACGBACACCCTGCAAGGAACCCTGCAAGGAACCCTCTCTGTGTACGBACACCCTGCAAGGACATCCTCTCTGTGTACGBACACCCTGCAAGGACATCCTCTCTGTGTACGBACACCCTGCAAGGACATCCTCTCTGTGTACGBACACCCTGCAAGGACATCCTCTCTGTGTACGBACACCCTGCAAGGACATCCTCTCTGTGTACGBACACCTGCAAGGACATCCTCTCTGTGTACGAAGAACCCTGCAAGGACATCCTCTCTGTGTACGAAGAACCCTGCAAGGACATCCTCTCTGTGTACGAAGAACCCTGCAAGGACATCCTCTCTGTGTACGAAGAACCCTGCAAGGACATCCTCTCTGTGTACGAAGAACCCTGCAAGAACCCTGCAAGAACCCTGCAAGAACCCTCTCTGTGTACGAAGAACCCTGCAAGAACCCTCTCTGTGTACAAGAACACCTGCAAGAACCCTGCAAGAACCCTCTCTCT	8 8
<b>_</b>	Query March 45.5; Score 662.2; DB 2; Length 178504; Best Local Similarity 99.79; Preds No. 8; e-128; Indels 1; Gaps	
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	misc_feature 1815130428	
	/note="assembly_fragment" misc_feature 1335618050	
	misc_feature 686013255	
	misc_feature 2484. 6759	
	misc_feature 12383	
	/organism=van rogicoyees* //organism=van rogicoyees* //organism=van rogicoyees* //organism=van rogicoyees* /clone=FR43-cSR10*	
	source 1. 178504	7
	* 132	2
	1 4795	
	44564 84779: contig of 4021	
	30529 44463: contig of 1393	
	30429 30528: gap of unknown	
	18051 18150: gap of unknown length	
	13256 13355: gap of unknown length	
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Center: Weblington University Genome Sequencing Center Center Code: WIDSC Visions Sequencing Center Center Code: WIDSC Visions Sequencing Center Project Information Center Project name: H. HROLOITII.  Center Project name: H. HROLOITII.  Sequencing vector: Maj 1004 Sequencing vector: Maj 1004 Sequencing vector: plasmid; 04 Chemistry: Dye-centinator Big Dye; 04 of reads Chemistry: Dye-centinator Big Dye; 04 of reads Chemistry: Dye-centinator Big Dye; 04 of reads Assembly Projectan: Phrap; version 0, 190119 Consensus quality: bases at least Qa0 Therr size: 13000; agardse-fp Insert size: 13000; agardse-fp Ouality coverage: 3.67 in Qa0 bases; sum-of-contigs Ouality coverage: 3.67 in Qa0 bases; sum-of-contigs  * is not known and their order in this sequence places  * is not known and their order in this sequence according at arbitrary. Gaps between the contigs are represented as	RSSUIT 12  ACCUSSION ACCIDIANS ACCIDIANS ACCIDIANS ACCUSSION ACCESSION ACCESSION ACCESSION ACCIDIANS ACCESSION ACCES	Oy 1116 GAMGCTRAMATGCAGGAMGTGGTAGGAMAGGTTTATTCCAGGAMGCAGGAMGCCAGGT 1175  Db 100075 GAMGCTGAMATGCAGGAMGTGGTAGGAMAGGTTTATTCCAGAGAMGCAGGAMGCCGGTC 110016  Oy 1176 ATCACCCAGCTCTGAGGAGCAGTTACTGCAGCTGACTTCCTCTGCCACTTC 1225  Db 108015 ATCGCCACCCTCTGAGGGAGCTACTGCAGCTCACCTCAC
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/clone="RP11-10111"

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ORIGIN
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Query Match 43.6%; Score 633.6; DB 2; Length 142334;
Best Local Similarity 98.8%; Pred. No. 8.3e-122;
Matches 680; Conservative 0; Mismatches 4; Indels 4;
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100266. 107334
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55676 CCTCCCCAGTCGGCTGAACTCTCCCCTTGTCTGCACTGTTCAAACCTCTGCCGCCCTCCA 55611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55736 GATCCAGATGITATGCTCCTGCTGATCCAGATGCCCAGAGGCTCCATCGTCCATCCTCTT 55677
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                                                                                             gene sets
Patent: WO 0194629-A 1678 13-DEC-2001;
Avalon Pharmaceuticals (US)
                                                                                                                                                      Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                             Homo sapiens (human)
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Sequence 1678 from Patent WO0194629,
AX331169
                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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      Query Match 35.0%;
Best Local Similarity 99.4%;
Matches 531; Conservative
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Sequence 208
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AX331572.1
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                                                                                                                                                                                                                                                                                                Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D. R. and Meaver, Z. Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                Homo sapians
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleoscomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                           gene sets
Patent: WO 0194629-A 2081 13-DEC-2001;
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Location/Qualifiers
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                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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      Score 508.4; DB 6
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AX335105
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Best Local Similarity

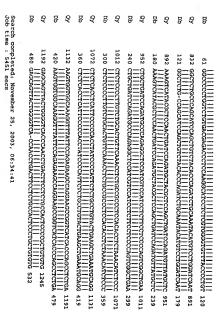
Matches 531; Conserv
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Sequence
AX335105
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Cancer gene determination
                                                                                                                                                                                        Patent: WO 0194629-A 5614 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
                                                                                                                                                                                                                                  gene sets
                                                                                                                                                                                                                                                            Young, P.E., Augustus, M., Carter, K.C., Horrigan, S., Soppet, D.R. and Weaver, Z.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.7e-95;
0; Mismatches 1
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# GenCore version 5.1.6 Copyright (a) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 25, 2003, 08:52:05; Search time E5 Seconds
('without alignments)
1294,955 Million cell updates/sec

Title: Perfect score: Sequence: US-10-021-368-1 1496 1 MRAPHLHLSAASGARALAKL.....AVYTQICKYMSWINKVIRSN 276

Scoring table: 830525 segs, 258052604 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

830525

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SPIREMBL 23:\* sp\_bacteria:\*
sp\_fungi:\*
sp\_numan:\* sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_arteriap:\*
sp\_archeap:\* sp\_organelle:\*
sp\_phage:\* sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

16	15	14	13	12	11	10	9	00	7	6	· UT	4	ω	N	-	Result No.
483	486	490	490	496	499.5	499.5	502	506	506	514	534	538	544	552.5	1028	Score
32.3	32.5	32.8	32.8	33.2	33.4	33.4	33.6	33.8	33.8	34.4	35.7	36.0	36.4	36.9	68.7	Query
247	254	275	246	246	276	246	250	276	249	255	249	253	260	234	278	Length DB
13	11		11	11	11	11	11	11	11	4.	11	4.	4	11	11	80
Q9W7Q5	Q8CGR4	QBIXD7	Q9Z1R9	Q9QUK9	Q8CGR6	Q9R0T7	Q8CGR5	Q9QYN3	Q9QYN4	Q96RQ0	Q91VE3	Q8N5N9	69MI80	Q9CV76	Q99M20	ID
Q9w7q5 paralichthy	Sna	Q8ixd7 homo sapien			Q8cgr6 mus musculu	mus	Snw	สมเร		Q96rq0 homo sapien	Q91ve3 mus musculu	OMO	Q8iw69 homo sapien	Q9cv76 mus musculu	_	Description

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### ALIGNMENTS

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                                                                                                                      Pfam, PRO0089; trypsin, I.
PRINTS; PRO072; CHWOTRYPSIN.
SMART; SM00020; Tryp, SPC; 1.
PROSITE; PS0040; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN H.55; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. EMBL; AK009217; BAB26143.1; -. HSSP; P00763; 1DPO.
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STRAIN-C57BL/6J; TISSUE-Tongue;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TYEMBLITE1. 17, Great
01-JUN-2001 (TYEMBLITE1. 17, Last
01-JUNA-2003 (TYEMBLITE1. 23, Last
2310008B01Rik protein (Fragment).
                                         Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1916761; 2310008B01Rik.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.020; -
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234 AA;
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25888 MW; 6D81E609EDD39110 CRC64;
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Query Match

36.9%;

Score 552.5;

DB 11; Length 234;

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QENSN9
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Best Local
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Matches 112; Conserv
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031M67-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
QaN5N9;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Straus
                                                                                                                                            Q8N5N9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
ernunum: 260 AA; 28090 мм; вр5934вв96295660 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                       262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 QCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQS
                                                                                                                                                                                                                                                                                                        24S ICRYLDWIKKIIGS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 KLARPVVÞGÞRVRALQLÞYRCAQÞGDQCQVAGMGTTAARRVKYNKGLTCSSITILSÞKEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 DSGGPLVCDETLQGILSWG-VYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 QLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 LIMAQUWAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 GVECVKNSQPWQVGLFHGKYLRCGGVLVDRKWVLTAAHCRDKYV-VRLGEHSLTKLDWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQ-GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                             ICKYMSWINKVIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                     EDAYPGQITDVMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAHCKKPKYTVRLGDHSLQNKDGPBQEIPVVQSIPHPCYNSSD----VEDHNHDLMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAHCGNKPLWARVGDDHLULLQG-EQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLGGAWAGHSR--AQEDKVLG----GHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSGGPLVCGGVLQGLVSWGSVGPCGQKGIPGVYTKVCKYTDWIRIVIRNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QURHTTFSITHPSY-QGA-----YQNHEHDLRLLRLNRPIHLTRAVRPVALPSSCVTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.7%;
                                                                                                                                                                                                                                                                                                                                                                  275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Mismatches 104; Indels
     Last sequence update)
Last annotation update)
                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.1e-45;
9; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 544; DB 4;
Pred. No. 8.5e-45;
                                                                                                                                       253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT S
Q91VE3
ID Q91V
      RARGER RESERVED ON CONTRACTOR OF THE PROPERTY 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                   091VB3;
01-DEC-2001 (TrEMELTE1. 19, Created)
01-DEC-2001 (TrEMELTE1. 19, Last sequence update)
01-DEC-2001 (TrEMELTE1. 2), Last sequence update)
01-MBC-2000 (TrEMELTE1. 2), Last sequence update)
filymolpsin (Scratum corneum chymotryptic enzyme) (Kallikrein 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Shmitted (UTW-2002) to the EMBL/GenBank/DDBJ databases.
1- SINLLARITY: BELONGS TO PETIDASE FAMILY S1.
EMBL, BC032005, ABM32005, 1; -; THE STANDARD FAMILY S1.
InterPro, IRR001314; Chymctrypsin.
InterPro, IRR001314; Chymctrypsin.
Therefor, IRR001314; Chymctrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PP00089; trypsin; I
PRANTS, PR00722; CHYMOTRYPSIN.
SMART, SM00020; Tryp, SRC; 1.
SMART; SM00020; Tryp, SRC; 1.
PROSITE; PS01040; TRYPSIN DOM, 1.
PROSITE; PS01034; TRYPSIN ESR; 1.
PROSITE; PS01035; TRYPSIN ESR; 1.
   Hansson L., Backman A., Ny
Wallbrandt P., Egelrud T.;
                                         STRAIN-129/SvJ;
                                                                                                                                    Yamaguchi N.;
"A novel cDNA
                                                                                                                                                                       TISSUE-Thymus;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kallikrein 7 (chymot
Homo sapiens (Human)
                                                                     SEQUENCE FROM N.A.
                                                                                                            Submitted (OCT-1997)
                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 chymotryptic, stratum corneum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 HVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFPSDLMCVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 DEHDIMILIKLARPVVPGPRVRALQLPYRCAQPGDQQQVAGWGTTAARRVKYNKGLTCSSI 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 ARALAKLIPLIMAQUWAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                        cDNA cloning of mouse serine protease, d (OCT-1997) to the EMBL/GenBank/DDBJ da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNDPGVYTQVCKFTKWINDTMKKH 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLISPQDCTKYKDLLENSMLCAGIPDSKKNACNGDSGSPLVCRGTLQGLVSWGTFPWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILSPKECEVFYPGVVTNNMICAGL-DRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLVNERWYLTAAHCKKMEYTVHLGSDTLGDRRAQRI-KASKSFRHPGY-----STQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQGEQLRRTTRSVVHPKYHQGSGPILPRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARSILLPLQILLISLALETAGEEAQGDKXID----GAPCARGSHPWQVALLSGNQLHCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease; Serine protease.
253 AA; 27608 MW; 2D68B6A41B22A668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (chymotryptic, stratum corneum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.0%; Score 538; DB 4; 40.5%; Pred. No. 3.1e-44
                        NY A.,
                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT,
                        Edlund M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.1e-44;
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                        Edholm E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98; Indels
                                                                                                        e, Thymopsin, i.";
databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 253;
                        Tornell J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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RESCOOR BARA
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Eukaryota; Metazoa;
Mammalia, Eutheria;
NCBI_TaxID=9606;
                                                                                                                                        01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                 Q96RQ0,
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MED; WGI.1346336; KLZ;
InterPro, IPRO1254; Seg_protesse_fry,
InterPro, IPRO1254; Seg_protesse_fry,
IFRANTS; PRO01254; Seg_protesse_fry,
IFRANTS; PRO0122; CHYMOTEVPSIN.
PROSITE; PS0124; TEVESIN, Dow; 1.
PROSITE; PS0124; TEVESIN HIS; 1.
PROSITE; PS0124; TEVESIN HIS; 1.
PROSITE; PS0124; TEVESIN ESR; 1.
PROSITE; PS0124; TEVESIN ESR; 1.
PROSITE; PS0124; TEVESIN ESR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Epidermal overexpression of stratum corneum emice; a model for Chronic ithchy dermatitis."; Submitted (JAN-2001) to the EMSL/GenBank/DDBJ databases.
                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1 - SHRILARIYY BELONGS TO PEPTIDASE PAMILY S1.
BHBL, ABORGS71, BABSSGOA, 1; -
BHBL, ABORGS71, BABSSGOA, 1; -
BHBL, BC027823, AAK27823, 1; -
BHBL, AK027447; BAC56467.1; -
BHBL, AK027447; BAC56467.1; -
BHBL, AK027447; BAC56467.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team, **Nax1/918 of the mouse transcriptome based on functional annotation 60,770 full-leagh cDNAs ". Reture 420:563-573(2002)
                                                                                                                  Frostinogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         225 PNDPGVYTQVCKYKRWVMETMKTH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 HVNDIMLVRLDEPVKMSSKVEAVQLPEHCEPPGTSCTVSGWGTTTSPDVTFPSDLMCSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 DEHDIMILKIARPVVPGPRVKALQIPYRCAQPGDQCQVAGWGT~AARRVKYNKGLTCSSI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P00761; 1AN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 LAKLLPLIMAQIMAABAALLPQNDTRIDPBAYGAPCARGSQPWQVSLFNGLSFHCAGVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                AQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILSPKECEVFYPGYVTANMICAGL-DRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLISSRECKKVYKD£LGKTMLCAGIPDSKTNTCNGDSGGPLVCNDTLQGLVSWGTYPCGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKYWVLTAAHCKMGQYQVQLGSDKI----GDQSAQKIKATKSFRHPGY-----STKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQSWVLTAAHCGNKPLWARVGDDHLLLLQGEQLR---RTTRSVVHPKYHQGSGPILPRRT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLSLITVLLS--LALETA--GQGERIID----GYKCKEGSHPWQVALLKGNQLHCGGVLV 56
                                                                                                                                        (TrEMBLrel. 19,
(TrEMBLrel. 19,
(TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                     PRELIMINARY;
                                   Chordata,
Primates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.7%; Score 534; DB 11; 40.2%; Fred. No. 7.6e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Mismatches
                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     PRT:
                                                                                                                                                                                                                                                     255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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SEQUENCE FROM N.A.

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RESULT 7
Q9QYN4
ID Q9QY
                         RAPAR REPRESENTATION OF THE PROPERTY OF THE PR
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Best Local
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MEDLINE-21085G9, PubMed-1121785,
Kawai J., Shinagawa A., Shibate X., Koshino H., Adachi J., Fuhuda
Arakwa T., Hata A., Puhumishi Y., Konno H., Adachi J., Fuhuda
Alizawa X., Tzawa M., Mishi K., Kiyosawa H., Kondo S., Yamamaka
Alizawa X., Tzawa M., Mishi K., Kiyosawa H., Kando S., Yamamaka
Alizawa X., Cawa H., Mishi K., Kiyosawa H., Kando S., Yamamaka
Alizawa X., Cawa H., Mishi K., Kiyosawa H., Kando S., Yamamaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
RCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-0907H;
01-087-2000 (TERMELEA! 13, Created)
01-087-2000 (TERMELEA! 33, Last sequence update)
01-088-2000 (TERMELEA! 33, Last annotation update)
11-088-2000 (TERMELEA! 33, Last annotation update)
11-088-2000 (TERMELEA! 35, Last annotation update)
11-08-2000 (TERMELEA! 35, Last annotation update)
11-08-2000 (TERMELEA! 33, Last annotation update)
11-08-2000 (TERMELEA! 34, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 40:1679-1687 (2001).
- SINILARITY: BELONGS TO PETIDASE PAMILY S1.
EMBL; AF930946; AAR62813.1; -.
HSSP; P00761; AM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostin, a novel
degenerate PCR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE=21226193, PubWed=11327827;
Takayama T.K., Cartee C.A., Deal antigen precursor (pro-PSA) by
"Activation of prosette-specific antigen precease identified by
prostin, a novel human prostatic serine protease identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9QYN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     "CDNA cloning of a novel brain serine protease, Hippostasin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        Mitsui S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACVVSGWGLVSHNEFGTAGSPRSQVSLPDTLHCANIGIISDTSCDKSYPGRLTNTWVCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JUL-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N., Mitsui
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255 AA; 27986 MW; 00D5B79E14B9468F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Yamagushi N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 514;
Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 AA
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RESULT 8
Q9QYN3
ID Q9QY

Q9QYN3 Q9QYN3; 01-MAY-2000 01-MAY-2000 01-MAX-2003

O (TrEMBLrel. 13, O (TrEMBLrel. 13, B (TrEMBLrel. 23, PRELIMINARY;

Created)

Last annotation update)

sequence update) 276 AA

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Mus musculus (Mouse). Hippostasin prostate PRSS20.

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

TISSUE-Prostate

N., Mitsui (JUL-1998)

S.; to the EMBL/GenBank/DDBJ

databases

TISSUE=Prostate;

SEQUENCE FROM N.A. Submitted Yamaguchi SEQUENCE FROM N.A. NCBI\_TaxID=10090

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BMELL ANDOISCAS DANSBEGS. 1.

BMELL ANDOPSEGU BARZEZGILI:

BMELL ANDOPSEGU BARZEZGILI:

BMEL ANDOPSEGU BARZEZGILI:

BMENSES, SOLIZST;

FERMESTED, ITRODIZSEJ, SER_DICEASE_TTY.

FERMESTED, SOLIZSTJ, FRESTU DOM. 1.

FROSITE, SOLOZAJ, TRYESIM DOM. 1.

FROSITE, SOLOZAJ, TRYESIM SER, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001)
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GDSGGPLVCNGSLQGIISWGQDPCAVTRKPGVYTKVCKYFNWIHEVMRNN
                                                                 SDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                               SCLISGWGTTSSPQLRLPHSLRCANVSIIEHKECEKAYPONITDTWLCASVRKEGKDSCQ
                                                                                                                                                                                                                                                                    QCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDR-GQDPCQ 226
                                                                                                                                                                                                                                                                                                                                                           QRRMATESEPHPDENNS----LENKDHRNDIMLVKMSSPVFFTRAVQPLTLSPHCVAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYECRPHSQPWQVALFQKTRLLCGATLIAPKWLLTAAHCRKPHYVILLGEHNLEKTDGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
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W; F9FF9CB457D727D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 506; DB 1
Pred, No. 4e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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MGD: MGI:1052971; PISSZO.

INTERPTO; IFR001114; Chymotrypsin.

INTERPTO; IFR001254; Set_protease_Try.

Ffam; PP00059; trypsin; i.

FRAINTS; PR00072; CHYMOTRYESIN.

SMART; SM00072; CHYMOTRYESIN.

SMART; SM000204; TRYPSIN_DMN; 1.

PROSITE; MS00114; TRYPSIN_MER; 1.

PROSITE; MS00114; TRYPSIN_MER; 1.

PROSITE; MS00114; TRYPSIN_MER; 1.
                                                                                                     SEQUENCE FROM N.A.
Adams M., Myral R.;
Adams M., Myral R.;
SUbmitred (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ANISA431, ANIFA421.1;
SEQUENCE 250 AA; 27016 WH; F62FEBF2290FEBES CR.O54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBCGR5,
                                                                                                                                                                                                                                                                                                                    Olsson A.Y., Lundwall A.; "Organization and evolution of the glandular kallikrein locus in Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Altua...

// ALX14.

Mus musculus (Mouse).

// Arvota; Metezoa; Chordata;

// Arvota; Metezia; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=22325484; PubMed=12437987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glandular
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                                                                                                                                                                                                                                                                                                            musculus."
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitsui S., Okui A., Kominami K., Vemuza H., Yamagushi N.;
*CDNA cloning and tissue specific splicing variants of mouse
hipposrasin/TuSP (PRSS20). *;
Blochim, Blophys. Acta 194:206-210 (2000).
-1- SINILARITY: BELOWGS TO PEPTIDASE PAMILY S1.
BBBL, ABGISS215;
-1- BILLARITY: BELOWGS TO PEPTIDASE PAMILY S1.
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                                      Local Similarity
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                                                                                                                                                                                                                                                                              Biophys.
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003 (TremBLrel. 23,
003 (TremBLrel. 23,
003 (TremBLrel. 23,
r kallikrein KLK14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDSGGPLVCNGSLQGIISWGQDPCAVTRKPGVYTKVCKYENWIHEVMRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCLISGWGTTSSPQLRLPHSLRCANVSIIEHKECEKAYPGNITDTMLCASVRKEGKDSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRRMATESEPHEDENNS----LENKDHRNDIMLVKMSSEVFFTRAVQPLTLSPHCVAAGT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLRRTTRSVVHPKYHQGSGFILPRRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protease; Serine protease.
276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                              Res. Commun. 299:305-311(2002)
    33.6%; Score 502; DB 11
39.8%; Pred. No. 9.9e-41
tive 43; Mismatches 9
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                      DB 11; Length 250;
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        Indels
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        18;
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Gaps
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RESULT 10
Q9ROT7
ID Q9R07
                                 RANK REPART OF THE PROPERTY OF
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RA Airawa K., Irawa M., Whinlishi Y., Konno H., Adochi J., Yamakuda S.,

RA Airawa K., Irawa M., Wishi K., Exyosuma H., Kondo S.,

RA Aisto T., Oscazaki Y., Golybbori T., Bono H., Kondo W.,

RA Kadola K., Matsudd H.A., Ashburnar M., Batellow S., Coasyvant T.,

RA Falschmann H., Gaarberland T., Gissi C., King B., Kochiwa H.,

RA Kuchi P., Lewis S., Matsuo Y., Mikaido I., Pecole G., Osackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Mikaido I., Pecole G., Osackenbush J.,

RA Sakirian L.M., Stanbii F., Suzuki R., Tomita M., Wagner L., Washio T.

RA Sakia K., Okido T., Furuno W., Aono N., Baldawelli R., Barah G.,

RA Blake J., Boffeill D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Blake J., Boffeill D., Hofmann M., Hume D.A., Kaniya M., Lee N. H.,

RA Oustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N. H.,

RA Oustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N. H.,

RA Wordone P., Harg S., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaii H., Sato K., Schoembach C., Saya T., Shinbata Y., Kotokuki S.,

RA Sasaii H., Sato K., Schoembach C., Saya T., Shinbata Y., Kotokuki S.,

RA Washina Forts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Ra Washina Forts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Ra Washina Forts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Ra Washina Forts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Ra Washina Forts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

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Ra Washina Forts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

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01-907-2000 (TEMBEREI. 13, Last sequence update)
01-907-2000 (TEMBEREI. 23, Last amnotation update)
Pancreatic crypsin (0910011191M protein) (Trypsinogen 8).
TD 08 0910011919K ON TRYPSINOGEN.
MEDIANA-21103195, PubMed-11160223,
Chen F., Rosen L., Hood L., Rothembarg E.V.,
"Differential transcriptional regulation of individual TCR Vbeta
                                                                                                                                                       STRAIN=129
                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Stomach,
MEDLINE=21085660; PubMed=11217851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kashiwabara S., Baba T.,
"A homologue of pancreatic trypsin is localized mammalian sperm and is released during acrosome J. Biol. Chem. 274:29426-29432(1999).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQACHRAYPGIITSGMVCAGVPEGGKDSCQGDSGGPLVCGGQLQGLVSWGMERCAMPGY
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Best Local S
Matches 108
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MED: MG1:913150; 0910001B19Rik.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Set protease_Try.
Pfam; PP00099; trypsin; I.
PRINTS; PR00725; CHYMOTRYESIN.
SMART; SMO0720; CHYMOTRYESIN.
SMART; SMO0720; Tryp_SPc; I.
PROSITE; MEDOS20; Tryp_SPc; I.
PROSITE; MEDOS20; Tryp_SPc; I.
PROSITE; MEDOS20; Tryp_SPc; II.
PROSITE; MEDOS20; Tryp_SPc; III.
PROSI
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1. SYMILARTY BELONGS TO BEFTIDASE PAMILY
BMBL, ABO17032 BAN4961.1.
BMBL, AKO03667; BAN25921.1.
BMBL, AKO03667; BAN2592542.1.1.
BMBL, AKO03664; AM859056.1.1.
   SEQUENCE FROM N.A.

Adams M., Mural R.,

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, MX152431, AAX79840.1, -.

SEQUENCE 276 AA; 30360 MM; 33E189C67492FDCA CRC64;
                                                                                                                                        Biochem.
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J. Immunol. 166:1771-1780(2001).
                                                                                                                                                                       musculus.
                                                                                                                                                                                          "Organization and evolution of the glandular kallikrein locus in
                                                                                                                                                                                                                    Olsson A.Y., Lundwall
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=22325484; PubMed=12437987;
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                  KLK13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8CGR6,
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SEQUENCE
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                                                                                                                                            Biophys. Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease; Serine protease.
246 AA; 26274 MW; B6A9F4C99079633F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.4%;
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                                                                                                                                            Commun. 299:305-311(2002)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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RESULT 12
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                                                                                                                                                                                                             RAMARIAT, Shinagawa A., Shinara K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Tawa M., Whunishi Y., Konno H., Adachi J., Puhuda S.,
RA Aiawa K., Izawa M., Mishi K., Kyosawa H., Kondo S., Yasanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bano H., Kando S., Yasanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bano H., Kandowa T., Salto R.,
RA Salto T., Okazaki Y., Salto R.,
RA Salta M., Watsada H.A., Ashburner M., Bacalov S., Casavant T.,
RA Salta M., Salta M., Rathburner M., Bara B., Kondow H.,
RA Salta M., Salta B., Salta M., Rathburner M., Wagner Que Wandho T.,
RA Schrint J., Washina S., Salta M., Garbaldo M.,
RA Salta K., Okido T., Furno M., Ason H., Badafeelli R., Barah G.,
RA Salta K., Okido T., Furno M., Ason H., Badafeelli R., Barah G.,
RA Salta K., Okido T., Furno M., Ason H., Badafeelli R., Barah G.,
RA Salta M., Bada M., Rathya M., Kaniya M., Lee M.,
RA Gustincich S., Hill D., Hofmann M., Hune D.A., Kaniya M., Lee M.,
RA Gustincich S., Hill D., Hofmann M., Skotfiguez J., Sakamoto N.,
RA Gustincich S., Hill D., Hofmann M., Skotfiguez J., Sakamoto N.,
RA Salta M., Saco K., Schembach C., Saya T., Shihata M., Scotchi K. F.,
RA Washaka-Borigo Oka Kiyang H., Washira M., Skotshi B.,
RA Washaka-Borigo Oka Kiyang H., Washira M., Skotshi B.,
RA Washaka-Borigo Oka Kiyang H., Washira M., Skotshi B.,
RA Washaka-Borigo Oka Kiyang H., Washira M., Skotshi B.,
RA Washaka-Borigo Oka Kiyang M., Hase M., Skotshi B.,
RA Washaka-Borigo Oka Kiyang M., Haseyam J., Kashira M., Kohashi B.,
RA Washaka-Borigo Oka Kiyang M., Baca M., Skotshi B.,
Ra Washaka-Borigo Oka Kiyang M., Baca M., Skotshi B.,
Ra Washaka-Borigo Oka Kiyang M., Baca M., Skotshi B.,
Ra Washaka-Borigo Oka Kiyang M., Baca M., Skotshi B.,
Ra Washaka-Borigo Oka Kiyang M., Baca M., Skotshi B.,
Ra Washaka-Borigo Oka Kiyang M., Baca M., Skotshi B.,
Ra Washaka-Borigo Oka Kiyang M., Baca M., Skotshi B.,
Ra Washaka-Borigo Oka Kiyang M., Baca M., Skotshi B.,
Ra Mayashi H., Skotshi B.,
Ra Mayashi H., Skotshi B.,
Ra Mayashi H., Skotshi M., Skotshi M., Skotshi B.,
Ra Mayas
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Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-39436155; PabMeda10506205;
Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S.,
Kashiwabara S., Baba T.;
Kashiwabara S., Baba T.;
Thomologue of pancreatic trypsin is localized in the acrosome
"A homologue of pancreatic trypsin is localized in the acrosome
mammallan sperm and is released during acrosome reaction.";
J. Blol. Chem. 27412446-29432(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                090UM5 PRELIMINARY; PRT; 246 AA.
090UM5-0 (TrebMire). 13 Created)
01-WAX-2000 (TrebMire). 13 Last sequence update)
01-WAX-2000 (TrebMire). 23 Last amotetion update)
TESP4 (0910001319RIK procein) (Trypsinogen 9).
TC 08 0910001319RIK OR TYPSINOGEN.
MEDLINE=21103195, PubMed=11160223; Chen F., Rowen L., Hood L., Rothenberg E.V. "Differential transcriptional regulation of
                                                                                                  [3]
SEQUENCE FROM N.A.
                                                                                                                                                     Nature 409:685-690(2001).
                                                                                                                                                                         "Functional anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTCCRVSGWGTTTSPQVNYPKTLQCANIELRSDEECRQVYPGKITANMLCAGTKEGGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGDQCQVAGMGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGL-DRGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQAMEVVRSIPHPEYQ-----VTPTHLNHDHDIMLLELKSPVQLSSHVRTLKLSADDCLP
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                                                                                                                                                                         annotation of a full-length mouse
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       individual TCR Vbeta
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SPEZILE 13

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0202189,
01-MAY-1999 (TrEMSLrel. 10, Created)
01-MAY-1999 (TrEMSLrel. 10, Last sequence update)
01-MAX-2093 (TREMSLrel. 23, Last annotation update)
Trypsinogen 16.
segments before gene rearrangement.";
                       Chen F., Rowen L., Hood L., Rothenberg E.V.; "Differential transcriptional regulation of individual TCR Vbeta
                                                                            MEDLINE=21103195; PubMed=11160223;
                                                                                                                       STRAIN=BALB/c;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Rowen L., Hood L., "Comparison between strains Balb/C and 129 in a region of the mouse
                                                                                                                                                                                                                                                                                                                            STRAIN=Balb/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRYGN16 OR TRYPSINGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9Z1R9
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PROSITE; PS00240; TRYPSIN DOW; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

SEQUENCE 246 AA; 26277 MM; 915029253E042809 CRC64;
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
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J. Immunol. 156:1171-1780(2001).

I. SINILARITY: BILONGS TO REPIDASE FAMILY S1.

RMEL, ABO03661, BAASS187.1.

BEBLI, ABO17031; BAASS187.1.

BEBLI, ARO17031; BAASS187.1.

BEBLI, ARO17031; BASS190.1.1.
                                                                                                                                                                                                         cell receptor beta locus.";
Submitted (NOV-1998) to the
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLMAQLWAABAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFLALVGAAVA--FPVDDD--DKIVGGYTCRENSIPYQVSLNSGYHF-CGGSLINDQWVV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EASYPGKITNNMICVGPLEGGKDSCQGDSGGPVVCNGQLQGIVSWG-YGCALKDNPGVYT
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                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
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41.0%; Pred. No. 3.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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RESULT 14
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    Matches 104;
                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROFS: 501.053:

MED: MGI: 2184749; Trygni6.
InterPro; JRR001314; Chymotrypain.
InterPro; JRR001254; Ser_pxtease_Try.
Pfam; PR00089; trypsin; 1.
PRLNTS; PR00722; CHYMOTRYESIN.
SMART; SM00722; CHYMOTRYESIN.
SMART; SM00726; Tryp_SPc; 1.
PR0SITE; PS00134; TRYP_SIN_DM; 1.
PR0SITE; PS00134; TRYPSIN_MER; 1.
PR0SITE; PS00134; TRYPSIN_MER; 1.
                         Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euthería, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variant form hippostasin/KLK11.
                                                                                                                                                                                                                                                                                             QSIXD7
                                                                                                                                                                                                                                                                                                         Q8IXD7
                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 32.8%; Score 490; DB 11; Length 246; Local Similarity 40.2%; Pred. No. 1.4e-39;
              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    261
                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 EVFYPGVVTNNMICAG-LDRGQDECQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 KLARPVVFGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKEC
                                                                                                                                                                                                                                                                                                                                                                           231 KVCNYVDWIQDTIAAN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 SAAHCYKTRIQVRLGEHNINVLEGNEQFIDAAKIIKHPNFN------RKTLNNDIMLI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 TAAHCGNKPLWARVGDDHLLLLQG-EQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 LIMAQIWAABAALIPQNDTRLDPEAXGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVL 82
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                                                                                                                                                                                                                                                                                                                                                                                                                           EASYPGKITGNMVCAGFLEGGKDSCQGDSGGFVVCNGELQGIVSWG-YGCALPDNFGVYT
                                                                                                                                                                                                                                                                                                                                                                                                  QICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLSSPVTLNARVATVALPSSCAPAGTQCLISGWGNTLSFGVSEPDLLQCLDAPLLPQADC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFLALVGAAVA--FPVDDD--DKIVGGYTCRENSVPYQVSLNSGYHF-CGGSLINDQWVV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 AA; 26134 MW; 34E173B18CA2F463 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease; Serine protease
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 43; Mismatches
                                                                                                                                                                                                                                                                                                         PRELIMINARY;
            32.8%;
  50; Mismatches
            Score 490; DB 4;
Pred, No. 1.6e-39;
                                                                                                                                                                                                                                                                                                         PRT;
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91; Indels
                         Length 275;
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  42;
Gaps
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19 KLLPLIMAQLWAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQ

RILQLILLAL----ATGLVGGETRI---IKGFECKPHSQPWQAALFEKTRLLCGATLIAP 54

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ID Q8CGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Adams M., Murah R., Saman M., Murah R., Samah R., Surah R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECURNCE FROM M A. MEDLINE-22325484; PubMed=12437987; MSDLINE-22325484; PubMed=12437987; Olsson A.Y., Lundwall A.; "Organization and evolution of the glandular kallikrein locus in Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus muscullus (Mouse).
Buraryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
Manmalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLK15.
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01-MAR-2003 (TrEMBLrel. 23, Created)

01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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229
                                                                                                                                                                                  192 SITILSPRESEVEYGOVTRANICAGID-ROODECOSDEGEFLYCDETLOGILSWGVYPC 250
                                                              251 GSAQHPAVYTQICKYMSWINKVIR 274
                                                                                                                                                                                                                                                                                                                                                                                    109 RLFKPARLTAYVRPVALPRRCPLIGEDCVVSGWGLLSDNNPGATGSOKSHVRLPDTLHCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 KLARPVVPGPRVRALQLPYRCAQPGDQCQVAGW-----GTTAARR--VKYNKGLTCS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 GEPLYCEFICGILSWGYYPGCSACHPAVTYQICKYNSWINKVIRN 276
229 GGPLYCNOSLQGIISWGQDPCAITRKPGVYTXVCKYTDMIQETMQN 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 TAAHCGREPHARVALOBHILLIAG-EQLERTTERVIJECYHOGSGPILFRRIDEHDJALL 141
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       DITTKPGVYTKVCSYLEWIWENVR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLAFVLLVSAA--QDGDKVLE----GEECVPHSQPWQVALFERGRENCGAFLISPRWVL 56
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Search completed: November 25, 2003, 09:08:42 Job time : 60 secs

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title: US-1 Perfect score: 1496 Sequence: 1 MR	Run on:
US-10-021-368-1 1496 1 MFAPHLHLSAASGARALAKLAVYTQICKYMSMINKVIRSN 276	November 25, 2003, 07:31:39; Search time 17 Seconds (763.492 Million cell updates/sec

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	<b>6</b> 0	7	•	us	Δ.	ω	ผ	Ļ	Result No.
452	457	457.5	458.5	460	464.5	467	468.5	468.5	469.5	470	477.5	481	482	483	486.5	488.5	488.5	494	497	497.5	499.5	500	502	503.5	505.5	506	513	520	547	549	564	1496	Score
30.2	30.5	30.6	30.6	30.7	31.0	31.2	31.3	31.3	31.4	31.4	31.9	32.2	32.2	32.3	32.5	32.7	32.7	33.0	33.2	33.3	33.4	33.4	33.6	33.7	33.8	33.8	34.3		g	36.7	37.7	100.0	Query
248	243	261	247	246	244	229	304	238	248	247	247	244	246	231	247	293	246	246	243	277	260	251	250	250	247	247	260	256	260	253	248	276	Length
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TRY1_CHICK	TRY1_XENLA	KLX7_RAT		TRY1_CANFA	TRY2_XENLA	TRYP SQUAC	TRY3_HUMAN	TRY3_SALSA	TRY3_CHICK	TRY2_HUMAN	TRY3_RAT	KLK6_HUMAN	TRY1_RAT	TRYP_PIG	TRY4_RAT	KLKS_HUMAN	TRY2_RAT	TRY2_MOUSE	TRY1_BOVIN	KLKO_HUMAN	NRPN_RAT	KLKE HUMAN	KLK9 HUMAN	KLKB HUMAN	TRY2 BOVIN	TRY2 CANFA	NRPN MOUSE	KLKF HUMAN	KLK8 HUMAN	KLK7_HUMAN			ID
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426.5	427.5	429	431.5	434.5	436	436	443	445.5	450.5	452	452	
28.5	28.6	28.7	28.8	29.0	29.1	29.1	29.6	29.8	30.1	30.2	30.2	
259	261	261	244	256	259	241	241	242	231	260	248	
<u> </u>	μ	۲	μ	-	۳	μ,	<b>,</b>	۳	μ	1	μ	
KLK9_RAT	KLK8 RAT	KTK6_MOUSE	KLKA_RAT	KLK4 MOUSE	KLKC RAT	TRYX GADMO	TRY1_GADMO	TRY1 SALSA	TRY2_SALSA	BSTA CANFA	TRY2_CHICK	
P07647 1												
rattus nor	rattus nor	muscul	rattus norv	mus musculv	rattus norv	gadus morhu	gadus morhu	salmo salar	salmo salar	canis famil	gallus gall	

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SEQUENCE PROM N.A. TISSUE-Tiesus, phymed-12477932; MEDLIFES-2388227, Phymed-12477932; Strambberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Stramberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	SEQUENCE PROM M. A.  Lamazdin J. E., McCready P. M., Skowtonski B., Viswanathan V.,  BawThart-Schultz K., Gozdon L., Dias J., Ramitez M., Stilwagen S.,  BawThart-Schultz K., Gozdon L., Dias J., Ramitez M., Stilwagen S.,  Phan H., Velasco N., Do L., Regala M., Terrys A., Brower A., Garnes J.,  Danganan L., Erler A., Christensen M., Georgeecu A., Avila J., Liu S.,  Andreise T., Trankheia M., Attix C., Amico-Kellar G., Coefisid J.,  Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  Areilano A., Gannaces C., Ow D., Nolan M., Trong S., Kobayashi A.,  "Sequence analysis of chromosome 1903.4.";  Submitted (OCT-2000) to the EMEL/GenBank/DDBJ databases.  [5]	SEQUENCE FROM N.A., Phylode-9647736; MIDLINE-9921710; PLANCE-9647736; MIDLINE-9921710; PLANCE-9647736; DEC. 1-7. BEATLY B., Squire J., DEC. 1-7. BEATLY B., Squire J., Squire J.	ANDATYCE; Metazos; Choroata; Cranata; vertebrata; Euteleoscom; kammalia; Eutheria; Primates; Catearthin; Hominidae; Homo. KERI_TAXID-9606; SIGNED ROWN, ANDATA ROWN, AND ROWN, A	IT 1  HIWAN  STANDARD, PRT; 276 AA.  043240, 999920, 9093W; 15-DEC-1998 (Real. 37, Last sequence update) 15-DEC-1998 (Real. 37, Last sequence update) 15-EEP-2003 (Real. 42, Last amoutation update) 15-EEP-2003 (Real. 42, Last amoutation update) 16-EEP-2003 (Real. 42, Last amoutation update) 18-EEP-2003 (Real. 42, Last amoutation update) 18-EEP-2003 (Real. 43, Last amoutation update) 18-EEP-2003 (Rea

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A lighthal S.F. Jacobarg B. Bletow K.H. Summan.

B. Hopkins R. Jocobar B. Wooder T. May S. Huster J. Haish P.

B. Distribenkoll. Metrusina K. Exrmer. May S. Huster G.M. Hong L. Scheetz T.E.

B. Stapleton M. Soares M.B. Sonaldo M.F. Casavant T.L. Scheetz T.E.

R. Brownstein M.J. Uschin T.B. Toshiyuki S. Carninci P. Prange C.,

R. Rahs S.S. Loquellano M.A. Peters G.J. Makek J.A. Gunarthen P. H.,

R. Bichards G. Worley K.C. Hale S. Garcia A.M. Guy L.J. Hallyk S.H.,

R. Bichards G. Worley K.C. Hale S. Garcia A.M. Guy L.J. Hallyk S.H.,

R. Millaid D. K. Muzzuy D.M. Sodergrun B.J. L. M. Globos R.A. SH.

B. Millaid D. K. Muzzuy D.M. Sodergrun B.J. L. K. Globos R. B.

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B. Milley R.M. Touchman J.M. Green E.D. Dickson M.C.

B. Blakesley R.M. Touchman J.M. Green E.D. Dickson M.C.

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B. Blakesley R.M. Touchman J.M. Green E.D. Dickson M.C.

R. Bodriguez A.C. Grimwood J. Schmatz J. Myess R.M.

R. Butterfield Y.S.M., Krzywinski M.I., Skalbska U., Smallus D.E.,

R. B. Ginerch A., Scheit J.E., Jones S.J.M. Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length

R.T. Human and mouse CDM soquences.
       DISULFID
CARBOHYD
CONFLICT
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PRINTS; PRO0727; CHYNOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00104; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HS; 1.

PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG
PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG
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EMBL; AF055481; AAC14266.1; --
EMBL; AF045527; AAG33363.1; --
EMBL; AC01473; AAG33356.1; --
EMBL; AC012710; AAH02710.1; --
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Goyal J., Smith K.M., Cowan J.M., Wazer D.E.,
"The role for NES1 serine protease as a novel
Cancer Res. 58.4882-4786 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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    - (- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.

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PROSTATE CAMEER
SUBCELLULAR LOCATION; Secreted (Probable),
TISSUE SPECIFICITY: EXPRESSED IM BERBAST, OVIARY AND
DEVELOPHENTAL STAGE: DOWN-REGULATED DURING BREAST
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16-OCT-2001 (Rel. 40, Created)
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16-OCT-2001 (Rel. 40, Last ann
16-OCT-2001 (Rel. 40, Last ann
SSOUBNC PROM N.A. (ISODOM 2).

Lamerdin J.E., McCready P.M., Stowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Stowronski E., Viswanathan V.,

Barkhart-Schultz K., Goxdon L., Das J., Ramirez M., Stilven N.,

Phan H., Velasco N., D. L., Regala W., Georgescu A., Avila J.,

Bunganan L., Erler A., Christensen M., Georgescu A., Avila J.,

Landraise T., Trambhein M., Attix C., Manico-Kaller G., Coefial J., Lilu

Buarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Sequence analysis of chromosome 19q13.4.",
                                                                                                                                                                                                                                                                                                                             Moss P., Paeper B., Wang K.; "Sequencing and expression analysis cluster located in chromosome 19q13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene 5 (KLK-L5).";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
YOUSE G.M., Magklara A., Scorilas A.
"Cloning of new alternatively spliced
gene 5 (KLK-L5).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999)
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Yousef G.M. Luo L.-Y. Diamandis E.P.;
"Identification of novel human kallikrein-like genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primares; Catarrhini; Hominidae; Homo.
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or (BC 3.4.21.-) (Kallikrein-like
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Scorilas A.,
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Pred. No. 2.1e-128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS50114; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 605539; ... G:extracellular; NAS. GO; GO:0005576; C:extracellular; NAS. GO; GO:0005609; P:proteolysis and peptidolysis; NAS. InterPro; IER001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                       Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Serine protease; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.020; -.
Genew; HGNC:6360; KLK12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF135025; AAD26426.2; -.
EMBL; AF135025; AAF06065.1; -.
EMBL; AF24527; AAG33365.1; -.
EMBL; AC011473; AAG23258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9UKR0-2; Sequence=VSP_005403;
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                         TPOCST.
                                                                   141
                                                                                         58
                                                                                                              82
                                                                                                                                                         23 LLMAQLWAAEAALLPQNDTRLDPEAY-GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9UKR0-1; Sequence=Displayed;
                                                                                                                                                                                         Similarity
   CHGYYPGRITSNNVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVY
                       CEVEXPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWG-VXPCGSAQHPAVX 259
                                                                   LKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKE
                                                                                         LTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-----TSHEHDLRL
                                                                                                              LTWAHCGNKPLWARVGDDHLLLLQ-GEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLML 140
                                              LRIRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHAT 171
                                                                                                                                    LLLCVLGLSQAA----TPK1FNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWV
                                                                                                                                                                                                                         248 AA;
                                                                                                                                                                               Conservative
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KALLIKREIN 12.

CHARGE RELAY SYSTEM

CHARGE RELAY SYSTEM

CHARGE RELAY SYSTEM
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                         Score 564; DB 1;
Pred. No. 5.4e-44;
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                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                         BB473E98F8BAF703 CRC64;
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Y SIMILARITY).
Y SIMILARITY).
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            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
European Bioinformatics Institute. There are no restrictions on
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P49862;
01-OCT-1996
01-OCT-1996
LINCHEM: BAODDYS RES. COMMUN. 211:586-589 (1995).

LINCTION: ANY CATALYZE THE DERABATION OF INTERCELLULAR CONTENUES STRUCTURES IN THE CORNITIONED LAYER OF THE SKIN IN THE CONTINUOUS SHEDDING OF CELLS FROM THE SKIN SHERAKE. SPECIFIC FOR ANNIO ACUD RESLIDUES WITH ACOMATIC SIDE CHAINS IN THE PL POSITION. SCCE CHAPES INTELLAN B CHAIN AT 6-LU-1-(-VS-7, 16-YR-1-JU-1), 25-PHB-1-TH-36, AND 26-TYR-1-TH-27, COULD PLAY A ROLE IN THE SKIN AND IS PRECURSORS TO INFLAMATORY CYNCHIES.

1- TISSUE SPECIFICITY: IT 18 ADMINIATIVE EXPRESSED IN THE SKIN AND IS LAXERSSED SHE MERCHANDER OF DEPLIBATION VERY LOW LEVELS ARE ALSO SEEN IN THE BRAIN AND KINDEY. PARTIC SHE CONTINUES AND SEEN IN THE BRAIN AND KINDEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skytt A., Stroemgvist M., Egelrud T.;

**Primary substrate specificity of recombinant human stratum corneum

**Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic ithchy dermatitis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Mose P., Pagper H., Mang K., Argonza-Barrett R., Lei H., McCuaig J.,
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 1943 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Openef G.M., Scorilas A., Diamandis B.P.; "Wolecular characterization, mapping and tissue expression of the "Wolecular characterization, mapping agene."; human stratum corneum chymotrypitc enzyme gene."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426 (1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kallikrein / precursor (EC 3.4.21.-) (Stratum corneum chymotrypric cnzyma) (hSCCB)
KALY OR PRSSG OR SCCE.
KALY OR PRSSG OR SCCE.
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15-SEP-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chymotryptic enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95314630; PubMed=7794273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
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PRINTS; PR00722; CHYMOTRESIN.
SMART; SM00020; Tryp_SE; 1.
SMART; SM00020; Tryp_SE; M.
PR05ITE; PS00134; TRYPESIN HDM; 1
PR05ITE; PS00134; TRYPESIN HSR; 1
PR05ITE; PS00135; TRYPESIN_SER; 1
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HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                       PNDPGVYTQVCKFTKWINDTMKKH
                                                                                                                                                                                                                                                                                                                                            KLISPODCTKVYKDLIENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQ
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
BY SHULARITY.
BY SIMILARITY.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      red. No. 1.36
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2D68B6B15A76A668 CRC64;
                                                                                                                                                                                                                                                                       252
                                                                                                                                                                                                                                                                                                             276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78)
78)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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Y SIMILARITY).
Y SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31
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                                               gene-14
                                                                 (Serine
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SEQUENCE OF 1-164 FROM N. A. (1806CRM 1).

Lamerdin J.E., NoCready P.M., Stoornoski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Skliwagen S.,

Phan H., Velasgo N., Do L., Regala M., Terry A., Erower A., Garnes

Danganan L., Erler A., Christensen M., Georgescu A., Osfila J., Liu

Madreise T., Trankheim M., Attix C., Anico-Keller G., Coefield J., Liu

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Sanders C., Ow D., Nalan M., Trong S., Kobayashi A.,

"Sequence analysis of chromosome 19q13.4.";

"Sequence analysis of chromosome 19q13.4.";

"Sequence analysis of chromosome 19q13.4.";

5 5

Arg-,

Lye-

AND

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Name=2

IsoId=060259-1; Sequence=Displayed;

splicing; Named isoforms=2

Isold-000259-2; sequence-VEP 005401;
TISSUE SECTIFICITY: ISOSOMN 1 IS RECOMBINANTLY EXPRESSED IN THE
BANCHEAS WHILE ISOSOMN 2 15 EXPRESSED IN NEIGHT BRAIN AND
BITPOCOMPUS: OPHT PORMS ARE ALSO FOUND IN FETAL BRAIN AND
PALCHMY. NOT DETECTED IN KINNEY, SPLESN, LIVER AND LUNG.
STALLMARTY: BECAMOS TO PETITOASE PAULY SI. KALIKKEIN SUBFAMILY.

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SEQUENCE FROM N.A. (ISOPORM 1).

Gan L., Geinnas R., Gown A.M., Moss P., Smith R., Wang K.,
Wholecular cloning and characterization of a novel serine protease,
Wholecular cloning and characterization of a novel serine protease,
Ovasin, a potential molecular marker for ovarian carcinomas.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  "Sequencing and expression analysis cluster located in chromosome 19q13
                                                                                                                                                                                                                                                                                                                                                           Moss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel form of human neuropsin, a br
generated by alternative splicing and
human adult brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein).
KLK8 OR P
                                                                                                                                                                                                                                                                                                                       Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                      Gan L., Lee I.,
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20510030; PubMed=11054574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serine protease overexpressed
Cancer Res. 59:4435-4439(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning of tumor-associated differentially expressed serine protease overexpressed by ovarian carcinoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Brien T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshida S., Taniguchi M., Hirata A., "Sequence analysis and expression of Gene 213:9-16(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Yerrebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
UPI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Underwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99413504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitsui S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99203457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Hippocampus;
MEDLINE=98372070; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLK8 OR PRSS19 OR TADG14 OR NRPN.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. 260:627-634(1999).
                                                                                                                                                                                                                                                                                                                                                         Paeper B., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203457; PubMed=10102990;
Tsuruoka N., Yamashiro
                                                                                                                                                                                                                                                                                                                                                                    Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10485494;
animoto H., Wang Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9714609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                    R., Argonza-Barrett R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K., Nakazato H., Yamagu
a brain-related serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                of the serine region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shiosaka S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shigemasa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rain-related serine protease, is expressed preferentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuropsin cDNA and
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                                                                                                                                                                                                                                                                                                                                           protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parmley
                                                                                                                                                                                                                                                                                                                                                                   McCuaig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene-14, a novel
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Best Local Sim
Matches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AB009649 RAA26673.11
EMBL, AB010790 BAA86804.11
EMBL, AB010790 BAA86804.11
EMBL, AB008937 BAA82665.11
EMBL, AB008937 BAA82665.01
EMBL, AB008937 BAA82667.01
EMBL, AB008937 BAA82367.01
EMBL, AB008937 BAA82367.11
EMBL, AB008937 BAA823874.11
EMBL, AB008937 BAA823874.11
EMBL, AB008937 BAA823874.11
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, P700089; trypsin, I.
PRINTS; PRO0722; CHMOTRYPSIN.
SMART; SW000702; Tryp. SPc; 1.
PROSITE; PS02040; TRYPSIN DOM; 1.
PROSITE; PS0114; PRVSIN HIS, 1.
PROSITE; PS00115; TRYPSIN_SER; 1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0007399; P:neurogenesis; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.244; -.
Genew, HGNC:6369; KLK8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase, Serine protease; Glycoprotein; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 605644;
                               262 ICKYMSWINKVIRS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q61955;
                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LLMAQLMAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                TAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSD-----VEDHNHDLMLL
                                                                                         EDAYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTN
                                                                                                                                           EVEXPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQ 261
                                                                                                                                                                                                                                                      KLAKEVVEGERVRALQLEYRCAQEGDQCQVAGWGTTAARRVKYNKGLTCSSITILSEKEC
                                                                                                                                                                                                                                                                                                                                                                  TAAHCGNKPLWARVGDDHLLLLQG-EQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLL 141
                                                                                                                                                                                                                                                                                                                                                                                                                        LLLGGAWAGHSR---AQEDKVLG----GHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVL
260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28048 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.6%;
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RY SIMILARITY

AUGUOSSIN.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

BY SIMILARITY.

BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 547; DB 1; Length 260;
Pred. No. 2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EF439E5B8C83E660 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 104; Indels
                                                                                                                                                                                                184
                                                                                                                                                                                                                                                                                                                                                                                                                        69
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"A novel serine proteinsse-like sequence from human brain.";
Blothim. Blothim. Acta 1218 225-228 (1994)

- FUNCTION: Protease whose physiological substrate is not yet known.

- SUBSELULAR LOCATION: Secreted (Frobable).

- AJTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=4;

IsoId=Q9H2R5-1; Sequence=Displayed;

ENBL, AP221295, AACO9469-11.

ENBL, AP221295, AACO9470-11.

ENBL, AP221295, AACO9471-11.

ENBL, AP221327, AAC93354-11.

ENBL, AP221327, ENBL, AE72580, ENBL,

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Isoid=09H285-4; Sequence=VSP\_005404;
-- TISSUE SPECIFCITY: Highest expression in the thyroid gland. Also expressed in the prostate, salivary, and adrenal glands and in the colon teetis and kidney.
--- SIMILARITY: BEDONGS TO PEPTIDASE FAMILY S1. KALLIKEEIN SUBFMHIY.

in the

IsoId=Q9H2R5-3; Sequence=VSP\_005406, VSP\_005407; IsoId=Q9H2R5-2; Sequence=VSP\_005405;

MEROPS; SO1.081; ".

GO; GO:0005576; C:sxtracellular; NAS.

GO; GO:0006508; P:pxoteolysis and peptidolysis; NAS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KuKr HUMAN STANDARD; PRT; 256 AA.
G9H2B5; Q15155; Q15123; Q15123; Q15124; Q2H2R; Q2H2R; Q2H2B5; g16-QCT-2001 (Rel. 40, Greated)
16-QCT-2001 (Rel. 40, Late sequence update)
18-PEP-2003 (Rel. 41, Late amnocation update)
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain; PubMed=8018728; MEDLINE=94289486; PubMed=8018728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McChaig J.,
Moss P., Reager B., Mangk A., Associated Restine protesse gene
Sequencing and expression analysis of the sprine protesse gene
cluster located in chromosome 1943 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20510030; PubMed=11054574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.F., Wolseular cloning of the human kallikrein 18 gene (KLKIS). Up-regulation in prostate cancer.", regulation in prostate cancer.", J. Biol. Chem. 276:53-61 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11010966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 ICRYLDWIKKIIGS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
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RESULT NEPA MO ID NR AC QG DT 15 DE NG QG MI QG 
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Best Local Sim
Matches 107;
SEQUENCE FROM N.A. "TISSUE-Hippocampus;
STRAIN-BALB/c, "TISSUE-Hippocampus;
MEDILINE-95348817; Pub/ded-7622137/Mmorta Y., Suzuki J., Tanaka T.,
Chen J. "L.", Yoshida S., Kato K.; Mometa Y., Shiosada S., Tanaka T.,
Chen J. "L.", Yoshida S., Kato K.; Mometa Y., Shiosada S., Tanaka T.,
"Expression and activity dependent Changes of a novel limbic-serine
"Expression and activity dependent Changes of a novel limbic-serine
                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
26-EEB-2003 (Rel. 41, Last sembtation update)
Neuropsin precourtor (EC 3.4.21.-) (NP) (Kallikrein LUKS OR PRESSIS OR NREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SI
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ACT_SI
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PROSITE: PS00134: TRYPSIN MIS .1
PROSITE: PS00135: TRYPSIN SER: FALSE NEG.
Hydrolase: Serine processe; Glycoprofein;
Alternative spiicing.
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRPN MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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InterPro; IPR001254; Ser_protease_Try.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCDNTTKPGVYTKVCHYLEWIRETMKRN 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCGSAQHPAVYTQICKYMSWINKVIRSN 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 520; DB 1;
Pred. No. 5.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP_005407.
SHNEPGTAGSPRSQ -> PLSSP (IN REF.
                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B5EBF8D6022786B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CCYSELD STRUCTURE Of BENIODSIN, a hippocampal protease involved in kindling epilepocamensis."

J. Biol. Chem. 274:420-424(1999).

J. Biol. Chem. 274:420-424(1999).

HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEDUTTIC ACTIVITY AGAINST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Hippocampus;
MEDLINE-99134351; PubMed-9933620;
Kishi T., Kato M., Shimizu T., Ka
Shiosaka S., Hakoshima T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skimaku C. Yoshida S. Shibata N. Kato K. Momota Y. Shioska T. Midorikawa R. Kamachi T. Kawaba A. Shi "Characterization of recombinent and brain meuropsin, plasticty-related serine processe.", Jasticty-72131109-7139(1998)
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                                                                                                                                                                                                                                                   PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp. SPc; 1.
PROSITE; PS00134; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_SER;
PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                               MREOPS, S01.244;
MREOPS, S01.244;
MRD: MGI-892018; KikB
InterPro, IRR001314; Chymotrypsin,
InterPro, IRR001354; Ser_protesse_Try,
Pfam; Pf00099; brypsin; l.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D30785; BAA06451.1; -. EMBL; AB032202; BAA92435.1; -. PIR; 156559; I56559.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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ENZYME REGULATION: STRONGIX INHIBITED BY DIISOPROPYL
FLUOROPHOSPHATE, LEUDEPTIN AND (4-AMIDINOPHENYL) METHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1NPM; 23-MAR-99.
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                                                                                                                                                                                                                               protease; Glycoprotein;
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                                                 NEUROPSIN.
CHARGE RELAY !
CHARGE RELAY !
                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAND
242 YTKICRYTTWIKKIM 256
              259 YTQICKYMSWINKVI 273
                              182 NKCERAYPGKITEGMVĆAGSSNGADTCQGDSGGPLVCDGMLQGITSWGSDPCGKPEKPGV
                                                               122
                                                                              139 MILKLARPVVPGPRVKALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSP 198
                                               199 KECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAV 258
                                                                                                                               13
                                                                                               67 WVLTAAHCKKOKYSVRLGDHSLOSRDOPEQEIQVAQSIQHPCYN-NSNP----EDHSHDI 121
                                                                                                              80 WYLTAAHCGNKPLWARVGDDHLLLL-QGEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDL 138
                                                                                                                                               20 LIPLIMAQIMAAEAALLIPQNDTRIDPEAYGAPCARGSQPWQVSLENGLSFHCAGVLVDQS 79
                                                                                                                                                                       Similarity
                                                              MLIRLQNSANLGDKVKPVOLANLCPKVGQKCIISGWGTVTSPQENFPNTLNCAEVKIYSQ 181
                                                                                                                               ILLLEMGAWA--GLTRAQGSKILE----GRECIPHSQPWQAALFQGERLICGGVLVGDR 66
                                                                                                                                                                                                260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
152
184
208
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                        45
47
53
55
65
67
72
72
110
100
110
1114
1114
1122
                                                                                                                                                                                                                                                                                                                                                                                        108
1115
1115
                                                                                                                                                                                                28523 MW;
                                                                                                                                                               34.3*, Score 513; DB 1; L
41.6*; Pred. No. 2.4e-39;
tive 32; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL) .
                                                                                                                                                                                                BE5F6F6BE37CD60E CRC64;
                                                                                                                                                                               DB 1; Length 260;
                                                                                                                                                                Indels
                                                                                                                                                               12;
                                                                                                                                                                Gaps
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RESULT 7

문 Ś 8 Ś 밁

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TRY2_CAM.

D'ATRY2_CAM.

D'ATR
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPRO01254; Ser_protesse_Try.
Pfam, Pf00089; trypein; 1.
PROMERY STATE STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its concent is fine commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ib-stb.ch/announce/or send an enall to license@ib-sib.ch/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the dog pancreas,";

Nol. Cell. Biol. 5:2659-2676(1985).

- OMPALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.

- SPECELULAR LOCATION: Extracellular.

- SMILARITY: BELONGS TO PEFTIDNSE PAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pinsky S.D., Laforge K.S., Scheele G.;
TDifferential regulation of trypsinogen mRNA translation: full-length
mRNA sequences encoding two oppositely charged trypsinogen isoenzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypsin, anionic precursor (EC 3.4.21.4). Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988
01-JAN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS, S01.258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M11589; AAA30899.1; -.
PIR; A26273; TRDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86284628; PubMed=3841794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CANFA
60 SAAHCYKSRIQVRLGEYNIDVLEGNEQFINSAKVIRHPNYNSW---IL----DNDIMLI 111
                                                                                                                                                                                                                                                                                                                  107,
                                                                               83 TAAHCGNKPLWARVGDDHLLLLQG-EQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLL 141
                                                                                                                                                                                                                            23 LLMAQLWAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVL 82
                                                                                                                                                         5 LILAFLGAAVAT--PTDDD--DKIVGGYTCEENSVPYQVSLNAGYHF-CGGSLISDQWVV 59
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
24
107
200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247
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                                                                                                                                                                                                                                                                                                                                                33.8%; Score 506; DB 1; Length 247; 41.8%; Pred. No. 9.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRYESIN, ANIONIC.
CHARGE SELAY SYSTEM
CHARGE SELAY SYSTEM
CHARGE PELAY SYSTEM
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374E9D31D6DB8EAF CRC64;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIFICITY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                  92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78)
78)
78)
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Y SIMILARITY).
Y SIMILARITY).
                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 8

PREZZ BOUND

AC Q2948 B

AC Q294
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                               Query Match
Best Local Simi
Matches 105;
                                                                                                                                                                                                                                        DISULFID
SITE
                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
PROPED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q29463;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPRO01254; Ser_protease_Try.

Pfam; PPO0089; trypsin; 1.

SMART; SM00020; Tryp_Spc; 1.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS0040; TRYPSIN DOW; 1.

PROSITE; PS01013; TRYPSIN HIS; 1.

PROSITE; PS01013; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
Typein, anionic precursor (RC 3.4.21.4).
Bos taurus (Bovine).
Bukaryote; Metasoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bumanyote; Metasoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bordate; Borine; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X54703; CAA38513.1; -. PIR; S13813; S13813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAINH-Soltesin-Friesian, TISSUE-Pancreas;
STRAINH-Soltesin-Friesian, TISSUE-Pancreas;
BERDLINE-91065383; POMOSd-1001417,
le Huerou I., Micker C., Gailloceau P., Toullec R., Puigeerver A.,
le Huerou I., Micker C., Gailloceau P., Toullec R., Puigeerver A.,
le Huerou I., Micker C., Gailloceau P., Toullec R., Puigeerver A.,
le Station and mucleocide sequence of cDNA clone for boyine
pancreatic anionic crypsinogen. Structural identity within the
trypsin family.";
ChrayTIC ACTIVITY; Preferential cleavage: Arg-[-Xaa, Lye-[-Xaa.-
- SUCCELLULAS LOCATION Excreenital cleavage: Arg-[-Xaa, Lye-[-Xaa.-
- SUCCELLULAS LOCATION Excreenital cleavage: Arg-[-Xaa, Lye-[-Xaa.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVCNFVDWIQSTIAAN 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENFYEOVYNNMICAG-LARGOPPOSDSGGFLVCDTLLGGLISMC-YGCLOAUXGGVTT

ENFYEOVYNNMICAG-LARGOPPOSDSGGFLVCDTLLGGLISMC-YGCLOAUXGGVTT

ENFYEOVYNNMICAG-LARGOPPOSDSGGFVCCNGELGGLISMC-YGCLOAUXGGVTT
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63
107
200
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48
132
139
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194
247
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                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease;
                                                                                                                                                                                                                                                                             107
200
160
160
233
233
236
236
                                                                    33.8%;
                                                                                                                                                                                                  26289 MW;
                                     42;
                                                                                                                                                                         ACTIVATION BEPTIDE
TRYSEIM, ANIONIC
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
BY SHILLARITY,

                                                                    Score 505.5; DB 1; Length 247; Pred. No. 1.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Digestion; Pancreas; Zymogen; Signal POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 AA
                                     156
                               Indels
                               15,
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260
                         6,
                         ZARAR REPERENCE BEREITER BEREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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                  Phan H.,
Danganan
Velasco N., Do L., Regala W.,
L., Erler A., Christensen M.,
Terry A.,
Georgescu
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		KTTT TO K		
FR 11005	520 OR TLSP.  (HAMMAI)  (H	230 TKVCNYVDWIQETIAAN 246  HDNAN  KLUS HDNAN  STANDARD; PKT; 250 AA.  GUBBT; 075837; QNNSS5; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last annotation update) 15-SEP-2003 (Rel. 42, Last annotation update) Mallikrein 11 Precursor (EG 3.4.21) (Hippostasin) (Trypsin-like	111 IKUSTENVINANUSTILLIPSKE 200 111 IKUSTENVINANUSTILLIPSKE 200 111 IKUSTENVINANUSTILLIPSKE 200 111 IKUSTENVINANUSTILLIPSKE 200 201 CEVERPOVTNANUSHA-LDROODERQASIGGEVUSTILGEVINANUSHAD 170 201 CEVERPOVTNANUSHA-LDROODERQASIGGEVUSTILGEVINANUSHAD 259 110 CENSTROOTINANUSHADELEROODERQASIGGEVINANUGHANUSHAD 110	

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RETURNING R. L., PERGY S. R., P
        Fram, PRO0089, trypsin, I.

PRINTS, PRO0122, CHHWOTKPENI,

PRINTS, PRO0122, THYP SPC; 1.

PROSITE, PRO0124, TRYPSIN DOW; 1.

PROSITE, PRO0134, TRYPSIN HIS; 1.

PROSITE, PRO0134, TRYPSIN SEE; 1.

PROSITE, PRO0135, TRYPSIN SEE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; SU1.2...
Genew; HGNC:6359; KLK11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, ABD12917; BAA33104.1, AM_IMIR.
EMBL, ABD13910; BAA88713.1.
EMBL, ABD13936; BAA98797.1.
EMBL, AF1642327; AAD37815.1;
EMBL, AF243227; AAD37816.1;
EMBL, AF243227; AAD37816.1;
EMBL, AF243227; AAD37816.1;
EMBL, AF243227; AAD37816.1;
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- TISSUE SPECIFCITY: EXPERSESSE IN BALM, SKIN AND PROSTRYE. 130FORM
1 15 EXPERSESSE DERFERRYTILLY IN BRAIN; 350FORM 2 IN PROSTRYE.
- SMILARIY: BELONGS TO DEPTINASE FAMILY 51. AMALIZHERIN SPERMILLY.
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Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kromiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Cerrano A.V.
Alternative splicing.
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S; S01.257; ..
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16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

28-FEB-2003 (Rel. 41, Last amocation updat

kallikrein 9 precursor (EC 3 4.21.) (Kall
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VARSPLIC
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Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Buteleostomi,
Mammalia: Butheria: Primates: Catarrhini: Hominidae: Homo.
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Anticancer Res.
                                                                                                                                                                                                        MRDLXMS=20118156; PubMed=1065253;
Yousef G.M., Luo L.-Y. Diamandis B.P.;
"Identification of novel human kallikrein-like genes
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192D910BBCDC7A56 CRC64;
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Yousef G.M., Diamandis E.P.; Growth and September 2 course the property of a new member, KLK-L3.";

SEQUENCE FROM N.A. MEDLINE=20247258; PubMed=10783266;

65:184-194(2000).

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Query Match
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Matches 104
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DISULFID
DISULFID
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ACT SITE
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DISULFID
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; P:proteolysis and peptidolysis; NAS.
InterPro; IPR001254; Ser protease_Try.
InterPro; IPR001254; Ser protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lamerdin J. B., NGCready P. M., Skowronski E., Viswanathan V.,
Burkhart-Genhir K., Gordon L., Dias J., Rants M., Skilween S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brows, A., Jarmes J.,
Danganan L., Erler A., Christensen M., Georgeou N., Owlai J.
Burtes P., Trankhein M., Artix C., Maioc-Reller G., Coffield U. S.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kromiller B.,
Areilano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
'Sequence analysis of chromosome 19013-1.",
Submitted (OCT-2000) to the EMBL/Genank/Dbg databases.

1- SUBCELULUAR LOCATION; Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PÉRAM, PRO0089; TYYDSIN, I
PRINTS; PRO072; CHYMOTRYPSIN.
SMART; SM00020, TTYD SPC; 1.
PROSITE; PS50240; TRYPSIN DOW; 1.
PROSITE; PS50240; TRYPSIN MIN; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SHISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformation and through a collaboration between the Caropaen Bioinformatics Institute. There are not the Swiss and the Swiss of the Caropaen Bioinformatics institute. There are not restrictions on its use by non-profit institutions as long as its content is in mo way modified and this statement is not removed. Usagg by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amounce/or send an email to licenses/ab-sib.ch/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:6370; KLK9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gan L., Lee I., Smith R., Argonza-Barrett R., Lei Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine cluster located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics
[3]
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           104;
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                                 Similarity
                                                                                                     250 AA;
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease;
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111
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164
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131
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                                                                                                                                              CHAGGE RELAY SYSTEM
CHAGGE RELAY SYSTEM
CHAGGE RELAY SYSTEM
BY SHILARITY
BY SHILARI
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                          Score
Pred.
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-LINKED (GLCNAC. ..) (P
-LINKED (GLCNAC. ..) (P
F2785245B063E98B CRC64;
           Mismatches
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                          2.3e-38;
                                                        DB 1;
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' SIMILARITY).
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LAKULPILMAQIMAABAALLPQNDTRIDPBAYGA-PCARGSQPWQVSIFNGISFHCAGVI

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RESULT 11
KLKE HUMAN
ID KLKE HUMAN
AC Q9POG3;
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           "Tissue-specific expression patterns and fine map kallkrein (KLM) Jocus on proximal 1943.4."

Biol. Chem. 275:37397-37406 (2000).

"SUCCELLILA LOCATION: Secreted (Probable).

"118UB SPECIFICITY: HIGH EXPRESSION IN BRAIN.

"537ML_LIVER. ALSO EXPRESSION IN LIVER, PAUGE.
                                                                                                                                                                                                                                                                         Lamerdin J.E., McCready P.M., Stouronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Diad J., Ramires M., Stilwsgen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garres
Danganan L., Erler A., Chistensen M., Georgeeu A., Avila J., Liu
hadreis G., Locas S., Bruce R., Thomas P., Quan G., Kochaller G.,
Arellamo A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
12 Clam A.S., Carrano A.V., 12 Clam A.S., Carrano A.V., Shirt Chicken C., Chicken 
                                                                                                                                                                                  MEDLINE=20545474; PubMed=10969073;
Harvey T.J., Hooper J.D., Myers S.A.,
                                                                                                                                                                      Clements J.A.,
                                                                                                                                                                                                                                       TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Genomics 73:117-122(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serine protease gene located on human in prostate and skeletal muscle. ";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE-1120997, PubMed=11352573;
HOOPER J.D., Bui L.T., Rae F.K., Harvey T.J.,
Ashworth L.K., Clements J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vousef G.M., Diamandis B.P.; Wolsed G.M., Diamandis B.P.; Wholocular characterization, mapping, and tissue expression a hormonally regulated kallikrein-like gene."; Submitted (UUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human
Eukaryota; Metazoa;
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28-FEB-2003
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   PROSTATE AND
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3 (Rel. 41, Last amnotation update)
14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6)
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SKELETAL
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Primates;
MUSCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome
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               PANCREAS,
                                                                                                                                    mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a novel kallikrein
me 19q13.4 and expressed
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               BONE MARROW AND S, FETAL SPLEEN,
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H
                                                                                                                                                                                  Ashworth L.K.,
                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of KLKL6,
                                                                                                                                    human
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.

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RESULT 12
NRPN RAT
ID NRPN
AC 08878
DT 15-JU
DT 15-JU
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DE Neuco
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Matches 97
NERN RAT STANDARD; PRT; 260 AA 089780; [15-JUL-1999 [Rel. 38, Creat sed] 15-JUL-1999 [Rel. 38, Leat sequence update) 26-FEB-2003 [Rel. 41, Leat amocation update Neuropeain precursor [EC 3.4.21.-] [WF] [Kol. protease 1].
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SMART; SMO0020; TYD, SPC; 1.
PROSITE; PS00240; TRYPSIN DM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SBR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00089; trypsin; 1. PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005508; P:proteolysis and peptidolysis; NAS.
InterPro; IPR001314; Chymotrypsin.
InterPro; TPR001254; Ser_protesse_Try.
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EMBL; AF283669; AAK48523.1; -.
EMBL; AF283670; AAK48524.1; -.
EMBL; AC011473; AAG23260.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS;
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                                                                                                                                                                                    COSDSGGPLYCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSWINKVIR 274
                                                                                                                                                                                                                                                                    TOOVLKVVROVTHENYNS-----RTHENDLMILGLOQPARIGRAVREIEVTQACASP
                                                                                                                                                                                                                                                                                                -EQLERTIRSVVHPKYHQGSGPILFRRTDEHDLMLLKLARFVVPGFRVRALQLFYRCAQF
                                                                                                                                                                                                                                                                                                                            GHTCTRSSQPWQAALLAGPRRRFLCGGALLSGQWVITAAHCGRPILQVALGKHNLRRWEA
                                                                                                                                                                                                                                                                                                                                                      GAPCARGSQPWQVSLFNG--LSFHCAGVLVDQSWVLTAAHCGNKFLWARVGDDHLLLLLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S01.029; -
                                                                                                                                                            COGDSGGPLVCRGQLOGLVSWGMERCALPGYPGVYTNLCKYRSWIEETMR
                                                                                                                                                                                                                GTSCRVSGWGTISSPIARYPASLQCVNINISPDEVCQKAYPRTITPGWVCAGVPQGGKDS
                                                                                                                                                                                                                                            GDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYFGVVTNNWICAGLDR-GQDF
                                                                                                                                                                                                                                                                                                                                                                                                                                           19
25
67
111
204
31
31
52
143
175
200
251 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                             27452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 33.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                    42.2%;
                                                                                                                                                                                                                                                                                                                                                                                     36,
                                                                                                                                                                                                                                                                                                                                                                                                  Score 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KALLIKREIN 14.
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal, Zymogen.
POTENTIAL.
ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           9087953BAFA7ED25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     ed. No. 3.5e-38
Mismatches 8
                       (Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
(BY SIMILARITY).
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                       8
                     (Brain serine
                                                                                                                                                                                                                                                                                                                                                                                   12;
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EVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQ 261 KLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKEC

**ERAYPGKITEGMVCAGSSNGADTCQGDSGGPLVCNGVLQGITTWGSDPCGKPEKPGVYTK** RLQNSANLGDKVKPIELANLCPKVGQKCIISGWGTVTSPQENFPNTLNCAEVKIYSQNKC

244 184 124 69 82

TAAHCGNKPLWARVGDDHLLLL-QGEQLERTTRSVVHPKYHQGSGPILPRRTDEHDLMLL 141 ILLPLLMGAWAGLTRAQGSKI----LEĞQECKPHSQPWQTALFQGERLVCGGVLVGDRWVL LLMAQLWAABAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVL

TAAHCKKOKYSVRLGDHSLQKRDEPEQEIQVARSIQHPCFN-SSNP

-EDHSHDIMLI

125 142 70 83

100, 13 23

Conservative

105;

Indels

9; Gaps

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Query Match
Best Local &
Matches 100
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PELMIS; PRO0722; CHYMOTRYPSIN.
SWART; SMO0020; TXYP_SEC; 1.
PROSITE; PESO240, TRYPSIN HOM; 1
PROSITE; PESO0134; TRYPSIN HOM; 1
PROSITE; PESO0135; TRYPSIN ESR; 1
                                                                                                                         DISULFID
DISULFID
CARBOHYD
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DISULFID
DISULFID
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ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
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                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and through a collaboration the European Bioinformatics Institute: There are no restrictions on its use by non-profit institutions as long as its content is in own way motified and this statement is no expense moved. Usegor by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an cmail to licensee@ibs-sib.oh).
                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease_Try.
Pfam; PF00089; trypsin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ005641; CAA06643.1; -. HSSP; Q61955; INPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Fischer, TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.244; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                             Similarity
                                                                                                                                            2120
212
39
58
145
152
                                                                                                                                                                                                                                                                                                                                                                                protease;
28
32
                                                                                                                                            173
173
246
246
233
                      33.4%;
                                                                                               28510
                                                                                            W.
                                                                                                              CHAGE RELAY SYSTEM
CHAGE RELAY SYSTEM
CHAGE RELAY SYSTEM
CHAGE RELAY SYSTEM
BY SIMILARITY.
Score 499.5;
Pred. No. 4e-3
38; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                            58DF4F0602A0B7F5 CRC64;
                         .5; DB 1;
4e-38;
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78)
78)
                                        Length
                                                                                                                  (POTENTIAL)
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Y SIMILARITY)
Y SIMILARITY)
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RESULT 13
KLKD_HUMAJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERDUENCE FROM N.A.
Lamerdin J.E., WcCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasgo N., Do L., Regala W., Terry, B. Bower, A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu N., Avila J. J.,
Andreise T., Trankhein M., Attix C., Anico-Keller G., Cocfield J.
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
Arelino A., Sanders C., Ow D., Wolan M., Trong S., Kobayashi A.,
"Sequence analysis of chromosome 19013.4";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
              Pfam; PF00089; trypsin; T.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                     GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006508; P:proteolysis and peptidolysis;
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                     This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.

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  Hydrolase,
                                                                                                                                                            MEROPS; S01.306; ...
Genew; HGNC:6361; KLK13.
MIM; 605505; ...
                                                                                                                                                                                                                EMBL; AF135024; AAD26425.2; -.
EMBL; AC011473; AAG23259.1; -.
EMBL; AL050220; CAB43320.1; ALT_INIT.
EMBL; AL050220; CAB43320.1; ALT_INIT.
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Submitted (MAY-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Uterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-180 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "dentification and characterization of Kuk-Lu, a new kallikrein-like
gene that appears to be down-regulated in breast cancer tissues.",
J. Biol. Chem. 275:11891-11899(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20229789; PubMed=10766816; Yousef G.M., Chang A., Diamandis E.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human),
Bukaryota; Medazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLK13 OR KLKL4
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16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
18-28-2001 (Rel. 41, Last annotation update)
18-18-2001 (Rel. 41, Last annotation update)
18-18-2001 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           orge W. Mirkner U., Mewes H.-W., Gassenhuber J., Wio
mitted (MAY-1999) to the EWBL/GenBank/DDBJ databases.
SECLEMULA LOCATION: SECRETED (Probable).
TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, BREAST, 1
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protease; Glycoprotein; Signal
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CONFLICT
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         215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
EGDSGGPLVCNRTLYGIVSWGDFPCGQPDRPGVYTRVSRYVLWIRETIR
                                                 QSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSWINKVIR
                                                                                                            TTCRVSGWGTTTSPQVNYPKTLQCANIQLRSDEBCRQVYPGKITDNMLCAGTKEGGKDSC
                                                                                                                                                                       DOCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGL-DRGODPC
                                                                                                                                                                                                                                                                                         QURRITES VVHPKYHQGSGPILPRETDEHDLMLLKLARPVVPGPRVRALQLPY-RCAQPG
                                                                                                                                                                                                                              QVREVVHSIPHPEYRRSPTHL----NHDHDIMLLELQSPVQLTGYIQTLPLSHNNRLTPG
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BY SI
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Pred. No. 6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BA8A9E8DCFB5D542 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Se-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                85;
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( SIMILARITY).
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                                                                                                                                                                                                                                  154
                                                                                                                                                                                                                                                                                         166
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TRY1 BOVIN P00760; 21-JUL-1986 01-NOV-1997 MEDLINE-75146445; PubMed=1092332; Titani K., Ericsson L.H., Neurath H., Walsh K.A.; "Amino acid sequence of dogfish trypsin."; "Covalent structure of bovine trypsinogen. remaining aridets.";
Bicchem Piantes."; Hartley B.S., MEDLINE=72035053; MEDLINB=67168848; PubMed=5967094; Mikes O., Holeysovsky V., Tomasek Submitted (OCT-1994) TISSUE=Pancreas; Okajima T., Maniwa M., Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Boyinae, Bos. (Fragment).
Bos taurus (Bovine). 01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Trypsinogen, cationic precursor (EC 3.4.21.4) BOVIN REVISIONS Homologies Biochem. SEQUENCE FROM N.A. NCBI\_TaxID=9913; 21-JUL-1986 (Rel. 01, Created) 01-NOV-1997 (Rel. 35, Last sec 15-SEP-2003 (Rel. 42, Last an SEQUENCE OF 15-243, AND DISULFIDE BONDS. Biophys. ă R. Soc. STANDARD; Res. PubMed=4399051; ö proteinases."; . Lond., B, Biol. Commun. Nagao S., Fujikawa H., o the EMBL/GenBank/DDBJ 24:346-352(1966) PRT; 243 Sci. 257:77-87(1970) ξ Goto S.; databases. (Beta-trypsin) position S.

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**Ranffean D.L.;

"The disulpida bridges of trypsin.";

"Mol. sbol. 12:299-992(1965).

1. KOL. STALVIIC ACTIVITY: Perferential cleavage: Arg-|-Xaa, Lys-|-Xaa.

1. CHALVIIC ACTIVITY: Skraecallular.

1. SUBCELLULAR LOCATION: Extraecallular.

1. TISSUE SPECIFICITY: SWIMSSIZED IN THE ACIMAR CELLS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This satiss-paper entry is copyright. It is produced through a collaboration between the Soliss Institute of Bloinformatics and the BMNE outstation. The Buropean Bloinformatics Institute. There are no restrictions on its use by non-posit institutions as Jong as its content is in no way modified and this statement is not removed. Usage by and for commercial multitus requires a license agreement (See http://www.iab-sib.ch/announce/or send an easil to licenses@abs-bib.oh/.
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     PD8
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Bode W., Schwaggar P.;
The refine ind crystal structure of boyine beta-trypsin at 1.8-A
resolution. IC Crystallographic refinement, calcium binding site,
benamidine binding site and active site at pH 7.0.";
J. Mol. Bol. 98:69-171(1975).
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08-NOV-88.
14-Mar-85.
16-APR-87.
15-APR-97.
14-MAR-85.
14-MAR-85.
15-APR-97.

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09-APR-85
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30-JAN-02

26-SEP-01. 26-SEP-01. 26-SEP-01. 26-SEP-01. 26-SEP-01. 26-SEP-01. 26-SEP-01. 26-SEP-01. 26-SEP-01. 1MTG 1MTG 1MTG 1MTG 1MTW 1TPS 1TYN 1TAW 1AQ7 1T10 2T10

> 14-OCT-96 20-AUG-97 12-NOV-97 12-NOV-97 12-NOV-97

11-NOV-98

IBTW 1BTX 1BTY 1BTZ 1JRS 1JRS 1JRT 1MAX

> 15-OCT-95. 15-OCT-95.

30-NOV-94

708.8 708.8

26-58F-01.
26-58F-02.
26-58F-03.

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P07146;
01-APR-1988
01-APR-1988
28-FEB-2003
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             This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                            elastase II and trypsin gense.",
Nucleic Acids Res. 14:8307-8330(1596).
- CAPALTYIC ACTIVITY: Preferential Cavarage: Arg-|-Xaa, Lys-|-Xaa
-- SIMPERLULAR ICONTION: BECENCEALLIAL
-- SIMILARITY: BELONGS TO PETIDASE PANILY S1.
                                                                                                                                                                                     MEDIAINE-87066713; PubMed-3641189;
Stevenson B.J. Hagenbuechie O. Wellauer P.K.;
"Sequence organisation and transcriptional regulation of
                                                                                                                                                                                                                                                               STRAIN=A/J;
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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European Bioinformatics Institute.
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22-JAN-02
23-FB8-02
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23-JAN-02
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(Rel. 07, Last sequence update)
(Rel. 41, Last annotation updat
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PRINTS, PRO0722; CHMOTRYPSIN
SMART, SMO00201 Tryp, SPG; 1
PROSITE; PSO0404 TRYBSIN DOM; 1.
PROSITE; PSO134 TRYBSIN HOS; 1.
PROSITE; PSO0135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.064; -.
MGD; MGJ:102759; Try2.
MGD; MGJ:RR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X04574; CAA28243.1; -.
EMBL; X04577; CAA28245.1; -.
FIR; B25528; B25528.
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SIGNAL 1
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231
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                                                                                                                                                                                                                                                         Similarity
                       QICKYMSWINKVIRSN 276
                                                                                                                                             SAAHCYKYRIQVRLGEHNINVLEGNEQFVDSAKIIRHENYNSW------TLDNDINLI
                                                                                                                                                                     TAAHCGNKPLWARVGDDHLLLLQG-EQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLL
 KVCNYVDWIQNTIADN
                                                                                                KLASPVTLNARVASVPLPSSCAPAGTQCLISGWGNTLSNGVNNPDLLQCVDAPVLPQADC
                                                                                                                                                                                              LILALVGAAVA--FPVDDD--DKIVGGYTCRESSVPYQVSLNAGYHF-CGGSLINDQWVV
                                             EASYPGDITWNMICVGFLEGGKDSCQGDSGGPVVCNGELQGIVSWG-YGCAQPDAPGVYT
                                                                      EVFYPGVVTNNMICAG-LDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYT
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 246
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TRYBEIN II. MIONIC
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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EX SMILARITY
EX SMILARITY
EX SIMILARITY
                                                                                                                                                                                                                                                       Score 494, DB 1;
Pred. No. 1.2e-37
                                                                                                                                                                                                                                                                                                          REQUIRED FOR SPECIFICITY (BY SIMILARITY).
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Search completed: November 25, 2003, 09:07:36
Job time: 19 secs

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

November 25, 2003, 08:58:10 / Search time 27 Seconds (without allgaments) 983.058 Million cell updates/sec

Run on:

Title: Perfect score: Sequence: US-10-021-368-1 1496 1 MRAPHLHLSAASGARALAKL.....AVYTQICKIMSWINKVIRSN 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

283308

283308 segs, 96168682 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	y,	4	3	2	1	No.	Result
439.5	443	445.5	445.5	450	450.5	453	457	457.5	458.5	460	464.5	467	468.5	468.5	469.5	470	473.5	477.5	482	483	486.5	488.5	491	494	505.5	506	513	549	Score	
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261	240	242	242	260	231	248	243	261	247	246	259	229	304	238	248	247	242	247	246	231	247	246	229	246				253	Length	
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ů	,	4	3	42	41	40	39	38	37	36	35	34	33	32	31	30
27.5	3	423	423	424	424	425	425	425.5	426.5	427.5	429	431.5	434.5	436	436	438
2.82	3	28.3	28.3	28.3	28.3	28.4	28.4	28.4	28.5	28.6	28.7	28.8	29.0	29.1	29.1	29.3
197	2	265	246	259	246	261	232	239	259	261	261	244	256	259	241	247
	,	_	N	۳	N	N	-	N	N	N	,	N	μ.	N	N	N
A25606	1	KORTP	JQ1472	KORTIN	JQ1471	A29745	KQPG	A27207	D23863	A34079	KQMS1	A44284	NGMSA	B31136	S39048	S12764
cissue kaliktein	1.27	tissue kallikrein	crypsin (EC 3.4.21	tonin (EC 3.4.21	trypsin (EC 3.4.21	tissue kallikrein	tissue kallikrein	tissue kallikrein	cissue kallikrein	tissue kallikrein	tissue kallikrein	tissue kallikrein	7S nerve growth fa	tissue kallikrein	trypsin (EC 3.4.21	trypsin (EC 3.4.21

#### ALIGNMENTS

RESULT 2 156559 neuropsin - mouse C:Species: Mis musculus (house mouse)	Oy  194 TILSEKSCEVETEGVYTNSMICHGL-DROGDEGGSBUGDETLGGILSHGVYBGGS 252  Db 169 KLISEQGCTKVYKOLLENSMICAGIEDSKYSNICKSDSGEFVCRGTTGGLVSHGTFEGG 228  OY 253 AGENTYPOTCKYMSHIKUTESN 276  Db 259 PHDROVYTQVKKTKNIKUTKKGI 252	Qy  74 TUJDOSWYLZAAHCGKELHARVGDDHILLIQGEQLARTTRSVHIPKYHQGSGFILPRRT 133  Db  58 TUVNERWYLTNAHCGONEYTYHLGDTIADRRACHAT-GASSFRHFOYSTQT 108  Qy  134 DEHDLALLKLARPVVFGPRVFALOLPTRCAQFGDQQQVAGMGTTAARRVKYNKGLTCSSI 193  Db  109 HYNDJHLYKLANGARLSSNAYKALBSKCEPGTTTTTSGMGTTTSDDTFFEDLMCTOP 168	Query Match  Gest Local Sinitarity 40.9%; Score \$49; DB 2; Length 253;  Best Local Sinitarity 40.9%; pred No. 17.2~40;  Matches 108; Conservative 45; Mismatches 97; Indels 14; Gaps 4;  Matches 108; Conservative 45; Mismatches 97; Indels 14; Gaps 4;  QY 14 ABALAKLI-FLAMAQIMANENALI-PONTELOPEN/VANCARGEOPHO/USEPICAG 73  Db 2 ARSILIPE/QILLISIALETHGEEN/GODKIID GAPCHROSHPWQVMLLSGNGLHOGG 57	A;Kolecule type: mBNA A;Residues: 1.253 +GNAN A;Crosa-references: GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504 C;Geneticn: C;Geneticn: GB:PSS65 -SCCB A;Gene: GB:PSS65 -SCCB A;Crosa-references: GB:377730 A;Map position: 7035-7035 C;Squestpailty: trypein typein bomology <try> F;30-245/Domain: trypein bomology <try></try></try>	Sayses serine pxoteinage SCCE precursor - human N;Alternate names: strutum corneum chymotryptic enzyme C;Becies: Hono saylans (man) C;Date: 07-011-1995 #sequence_revision 07-011-1995 #text_change 22-Jun-1999 C;Accession: A59968 R;Hansson, L.; Stroemgvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, J. Blol. Chem. 269, 19420-19436, 1949 A;Bite Cloning, expression, and characterization of stratum corneum chymotryptic enz A;Beterence number: A59968; MUID:94308225; PMID:8034709 A;Accession: A53968
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h, Molecule type: mRNA
A, Residues: 1.247 cPIN-
C, Serwoods: Mydrolase; pancress; protein digestion; serine proteinase; rymogen
C, Serwoods: Mydrolase; pancress; protein digestion; serine proteins
F, 1.257/Domain: activation populae #sextus predicted dAPT-
F, 1.257/Domain: signal sequence | Mydrolase; producted dAPT-
F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypein (SC 3-4.21-4) precureor, anionic dog
N.Alerante names cationic trypinogen
Cispecies: Canis lupus familiaris (dog)
Cispecies: Oranje-1997 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A28273
R;Pinsky, S.D., LaRorge, K.S.; Scheele, G.
MOI. Cell: Biol. 5, 2669-2676, 1985
A;Thits: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque
A;Reterence number: A28273; MUID:86284638; PMID:3841794
A;Reterence number: A28273; MUID:86284638; PMID:3841794
A;Reterence number: A28273; MUID:86284638; PMID:3841794
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C.Sauperfemily: crypsin tyrpsin homology
F;33-252/Domain: trypsin homology <TRY>
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R.Chen, Z.L., Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito
M. Rhen, Z.L., So88-6997, 1995
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A;Molecule type: mRNA
A;Residues: 1-260 <RES>
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A; Reference number: I56559; MUID:95348817; PMID:7623137
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                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 YTKICRYTTWIKKIM 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 KECEVFYFGVVTNIMICAGLDRGQDFCQSDSGGFLVCDETLQGILSWGVYFCGSAQHPAV 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
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                                                                                                                                                                                                                                                                                               107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 LIPTIMAQIWAAEAALIPQNDTRIDPEAYGAPCARGSQPWQVSIFNGLSFHCAGVIVDQS
               83 TAMHCGNKPLWARVGDDHLLLLQG-EQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLL 141
                                                                                                                                                                                     23 LIMAQIWAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSPHCAGVLVDQSWVL 82
                                                                                                  5 LILAFLGAAVAT--PTDDD--DKIVGGYTCEENSVPYQVSLNAGYHF-CGGSLISDQWVV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 34.3%; Score 513; DB 2; Length 260; Similarity 41.6%; Pred. No. 2.4e-37;
                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WVLTAAHCGNKPLWARVGDDHLLLL-QGEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDL 138
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                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                     33.8%; Score 506; DB 1; Length 247; 41.8%; Pred, No. 9.3e-37;
                                                                                                                                                                                                                                                                                       41; Mismatches
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                                                                                                                                                                                                                                                                                       92; Indels 16; Gaps
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                                     trypsin (GC 3-4.21.4) precursor - mouse Capecias: Num suscilus (Nouse mouse) Capace: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999 C.Paccession: B25588 Requence_revision 40-Jun-1988 #text_change 22-Jun-1999 R.Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K. Nucleic Acids Res. 44, 8307-8330, 1986 Res. 44, 8307-8330, 1986 Res. 44, 8307-8330, 1986 Res. 44, 8307-8330, 1986 Res. 45, 1215 Research number: A33646, MUID:87066713, PMID:8641189 A.Reference number: A33646, MUID:87066713, PMID:8641189 A.Reference number: A33646, MUID:87066713, PMID:8641189 A.Reference number: A33646, MUID:87066713, PMID:3641189 A.Reference number: A33646, MUID:87066713, PMID:3641189
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A. Title: Isolation and muchactide sequence of cDNA clone for bovine pancreatic anionic A. Reference number: $33813; BVIII:91065383; PMID:1701147
A. Accession: 213813
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C. Superfemily: trypsin broadbay
C. Keywords: bydrolase; protein digestion; serine proteinase
C. Keywords: bydrolase; protein digestion; serine proteinase
F:24-239/Domain: trypsin broadbay - KRYs
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A;Molecule type: mRNA
A;Residues: 1-247 <HUE>
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C:Dates Oz-De-1991 #sequence_revision 03-Mug-1995 #text_change 22-Jun-1999
C:Dates (Oz-De-1991 #sequence_revision 03-Mug-1995 #text_change 22-Jun-1999
C:Dates (Oz-De-1991 #sequence_revision 03-Mug-1995 #text_change 22-Jun-1999)
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 TKVCNYVDWIQETIAAN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 CENEYPGUVINNICAG-LORGODPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 IKLSTPAVINARVSTLLLPSACASAGTECLISGWGNTLSSGVNYPDDLLQCLVAPLLSHAD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 LKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKE 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 LTAAHCGNKPLWARVGDDHLLLLQ-GEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLML 140
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CiSpecies: Bos primigenius taurus (cattle)
CiSpecies: A4-Apr.1984 fleequence.revision 28-Peb-1986 #text_change 18-Jul-1997
CiAccession: A90144; A00464; 508074.
R/Mices of, Holsycoveky, V. Tomasek, V., Sorm, F.
Blochem, Blophys. Res. Commun. 24, 346-352, 1966.
A/Richem. Schopkys. Res. Commun. 24, 346-352, 1966.
A/Richem. Covalanc Structure of bovine trypsinogen. The position of the remaining amides.
A/Reference number: A90144; WUID:67168848; PMID:5967094
A/Reconstant. 390164
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C:Superfamily: trypsin sequence states protein digestion; serine proteinase
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F1: 24/S/Domain; signal sequence states predicted «SIG»
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A;Reference number: A93758
A;Contents: annotation; revisions
R;Titani, K. Bricesson L. H.; Waurath, H.; Walsh, K.A.
Bichemistry 14, 1358-1366, 1978
A;Richemistry 14, 1358-1366, 1978
A;Richemistry 14, 1358-1366, 1978
A;Reference number: A0589; MJD:75166445; PMID:1092333
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R,Hartley, B.S.
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A, Residues: 1-57, 'Q', 59-67, 'Q', 69-150, 'N', 152-176, 'N', 178-229 <MIK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trypsin (EC 3.4.21.4) precursor - bovine
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A;Cross-references: GB:X04574; NID:g54918; PIDN:CAA28243.1; PID:g54919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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F;7-131,132-229/Product: alpha-trypsin #status experimental kMT2.
F;6-7/Cleavage stee: Lys-11e (enteropeptidase) fractus experimental F;13-143,31-47,115-216,122-189,154-186,179-203/Picutifet bonds: #status experimental F;145-99,184/Active stee: His-Asp, Ser #status experimental Giu/#status experimental F;53-60,33-68/Binding stee: calcium (Giu/Asn, Val, Giu/#status experimental F;131-132/Cleavage sizes: Lys-Ser (autolytic) #status experimental
181 GÓSGGPVVCSGKLÓGIVSWG-SGCAQKNKPGVÝTKVCNÝVSWIKQTIASN
                                                                                                        227 SDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                 168 QCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAG-LDRGQDPCQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 QLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 GYTCGANTVPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHLLLLLQG-E 107
                                                                                                                                                                                                                        QCLISGMGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFISASKSIVHPSYNS-----NTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.8%; Score 491; DB 1; Length 229; 41.7%; Pred. No. 1.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84; Indels 12;
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# CiSpectses: Rattus norvegitus (Norwsy xt) CiDates GF-Apr-1983 #equence\_revision 30-sep-1987 #text\_change 18-Jul-1997 CiDates GF-Apr-1983 #equence\_revision 30-sep-1987 #text\_change 18-Jul-1997 CiAccession: A22657, A00949 RiCTalk, C.S. (Thoo, Q.L., Swift, G.H., Quinto, C.; MacDonald, R.J., Rutter, W.J. Biol. Chem. 259, 14255-14264, 1984 A;fielsersorie number: A22657, MUID:8504880; PMID:6094547 A;factescric number: A22657, MUID:8504880; PMID:6094547 A;factescric number: A22657

A,Wolsetile type: DNA A,Wolsetiles: 1-246 CCRA-R,MocDonald, R.J.; Stary, S.J., Swift, G.H. I, MocDonald, R.J.; Stary, 8.2, 1982 I, Bhol. Cohem. 257, 9724-9732, 1982 A,Fifther Two Similar but nonalielic rat pancreatic trypsinogens. Nucleotide sequences A,Fefference number: A00948; MUID:82265824; PMID:6896710 A,Fefference number: A00948; MUID:82265824; PMID:6896710 C; Comment: The trypsin II mRNA is present in much lower quantities than the trypsin I

C: (Superimally: trypsin) trypsin homology
C: (Superimally: trypsin) trypsin homology
F:1-15/(Domain signal sequence status predicted <5/30>
F:16-23/(Domain signal sequence status predicted <5/30>
F:16-23/(Domain signal sequence status predicted <6/30>
F:16-23/(Domain stivation peptide status predicted <6/30>
F:24-24/(Product: trypsin II #status predicted <6/30>
F:24-24/(Product: trypsin II #status predicted F:24-26/(Product: trypsin II #status producted F:24-26/(Product: trypsin II #status

Score 488.5; DB 1; Length 246; Pred. No. 3.1e-35;

15 RALAKILPILMAQIMAABAALIPQNDTRIDPBAYGAPCARGSQPWQVSLFNGLSFHCAGV 74 RAL-----LFLALVGAAVA--FPVDDD--DKIVGGYTCQENSVPYQVSLNSGYHF-CGGS 51 43; Mismatches 95; Indels 21; Gaps 8

75 LVDQSWVLTAAHCGNKPLWARVGDDHLLLLQG-EQLRRTTRSVVHPKYHQGSGPILPRRT 133

52 LINDOWVVSÄÄHCYKSRIOVRLGEHNINVLEGDEOFINAAKIIKHENF-----DRKT

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trypsin (SC 3.4.21.4) procursor - pig (tentative sequence)
NiContains trypsinogen
CiSpecies: Nus scroot consestic (domestic pig)
CiDates: 24-Apr-1944 Heoquence revision 24-Apr-1984 Htext_change
CiAncession: A90641; A90368; A00947 A.; Desmuelle, P.
Biochim. Biophys. Acta 69, 135-129, 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A/Cross-references: BMBL:X15679, NID:g56813, PIDN:CAA33718.1; PID:g56814
C/Superfamily: trypsin; trypsin bomology
Cyteywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen
F/1-15/Domain: signal sequence #status predicted c870s
F/1-15/Domain: activation peptide #status predicted APTy
F/2-427/Piroduct: trypsin IV #status predicted APTy
F/2-427/Piroduct: trypsin IV #status predicted cMATy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rijusecke, B.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.P. Nucleic Acids Res. 17, 6756, 1989
Nyfille: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.
A;Reference number: 805494; MUID:89386010; PMID:2780302
A;Accession: 805494.
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WAlternate names: 2X protein, trypsingen IV precursor
Cispecies: Rattus norvegicus (Norway rat)
Cipace: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Jun-1999
Ciaccession: 305194
                                                                                                                                                                          TRPGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:24-440/Domain: trypšin homology <PRÝy
F:30-161,49-65,133-34,40-207,13-186/Disulfide bonds: #status predicted
F:30-161,49-65,133-34; Adv-207,13-186/Disulfide bonds: #status predicted
F:76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-247 < LUE>
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                                                                                                                                                                                                                                                                                                        259
                                                                                                                                                                                                                                                                                                                                                    171
                                                                                                                                                                                                                                                                                                                                                                                        200 ECENEYPGYVTNIMICAG-LDRGQDPCQSDSGGPLVCDETLQGILSWGYYPCGSAQHPAV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                              111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LPLLMAQLWAAEAALLPQNDTRLDPEAYGAPÇARGSQPWQVSLFNGLSFHÇAGVLVDQSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102;
                                                                                                                                                                                                                                                                                                        YTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                SCKKSYPGQITSNMFCLGFLBGGKDSCDGDSGGPVVCNGEIQGIVSWGSV-CAMRGKPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                           LIKLKSPAVLNSQVSTVSLPRSCASTDAQCLVSGWGNTVSIGGKYPALLQCLEAPVLSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISIEFĀFĒGĀĀVĀ--LĒVNDD--DKIVGGYTCPKHLVĒYQVSLHDGISHQCGGSLISDQW 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLTAAHCGNKPLWARVGDDHLLLLQ-GEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILSPKECEVFYPGVVTWNMICAG-LDRGQDPCQSDSGGPLVCDETLQGILSWCVYPCGS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDNPGVYTKVCNYVDWIQDTIAAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNNDIMLIKLSSPVKLNARVATVALPSSCAPAGTÖCLISGWGNTLSSGVNEPDLLOCLDA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEHDLMLLKLARPVVPGPRVRALQLFYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACHPAVYTQICKYMSWINKVIRSN 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 486.5; DB 2;
Pred. No. 4.7e-35;
4; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
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Ajboce; at position 20; Ile and Val occur alternatively Cisuperfamily: trypsin trypsin bendony.
Cisupwords: hydrolass; pancreas; polymorphism; protesin digestion; serine profile protesing the control of the control o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 1-10 <CHA>
R; Hermodson, M.A.; Ericeson,
Biochemistry 12, 3146-3153, J
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A; Residues: 9-231 <HER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Su le trypsinogene
A;Reference number: A90641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                           123 ECLISGWGNTKSSGSSYPSLLQCLKAPVLSDSSCKSSYPGQITGNMICVGFLEGGKDSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GYTCAANSIPYQVSLNSGSHF-CGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQG-E 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
GDSGGPVVCNGQLQGIVSWG-YGCAQKNKPGVYTKVCNYVNWIQQTIAAN 231
                                                                                                             SDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                        QCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAG-LDRGQDPCQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFINAAKIITHPNFN-----GNTLDNDIMLIKLSSPATLNSRVATVSLPRSCAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLERTTRSVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.3%;
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Pred. No. 8.8e-35;
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C./Accession: B22657; A00348

G/Craik, C.S., Choo, Q.L., Swift, G.H., Quinto, C., MacDonald, R.J., Rutter, J. Biol. Chem. 259, 1255-14364, 1984

J. Biol. Chem. 259, 1255-14364, 1984

A;Tille: Structure of two related rat pancreatic trypsin genes.

A;Reference number: A22657; MUID:85054880; PMID:6094547

A;Accession: B22657
                                                                                                                                                                                                                              trypein (BC 3-4.21.4) I precursor - rat
NiAlestrate names: crypsinogen: NiAlestrate norvegicus (Norway rat)
CiSpecias: Natus morvegicus (Norway rat)
CiDate: 17-Dec-1502 Hequence_revision 17-Dec-1502 #text_change 24-Sep-1550
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W.J.

A; Molecule type: DNA A; Residues: 1-246 < CRA>

A)Cross-references: 0B:000778, NID:9206507, PIDN:AAA98519.1; PID:9206508
A)More: the authors translated the codon ATC for residue 6 as Leu and GAC for residue
R)MocDonald, N.J. Stary, S.J., Swift, G.H.
U. Biol. Chem. 257, 9724-9732, 1882
A)Filte: Two similar but nonalielic rat pancreatic trypsinogens. Nucleotide sequences
A)Fetternce number: A00948; MUID:82265624; PMID:6896710
A)Accession: A00948

A; Molecule type: mRNA A; Residues: 1-246 < MAC>

A;Cross-references: GB;J00778; NID:g206507; PIDN:AAA98518.1; PID:g206506 C;Genetics:

A.introms: 14/1.67/2; 152/1; 197/3 C:Superfamily: trypsin, trypsin homology C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen F;1-15/Domain: signal sequence fistatus predicted <81G>

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AlRedenile type: mRNA
AlRedeniues: 1-247 - CHES
AlRedeniues: 1-247 - CHES
AlRedeniues: 1-247 - CHES
C. Superfamily: trypein; trypein homology
C. Superfamily: trypein; trypein homology
C. Keywords: calcium binding; hydrolese; protein digestion; serine proteinase
F:25-240/Domain trypein homology cffs:
F:25-240/Domain trypein homology cffs:
F:25-240/Domain trypein homology cffs:
F:25-240/Domain trypein homology cffs:
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Blochenksty, J. 3031-3086, 1997
A.Fitler Isolation and characterization of a DNN encoding rat cationic trypsinogen.
A.Fatterene number, A2547, MUID:97271609; PMID:3607011
A.Facteresion. A2747.
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C.Species: Ratteu morvegicus (Norway XII-)un-1988 #Fext_change 22-Jun-1999
C.Dates 30-Jun-1988 #sequence_revision 30-Jun-1988 #Fext_change 22-Jun-1999
C.Nacesss:on A.27547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;64,108,201/Active site: His, Asp, Ser #status predicted F;76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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A27547
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                                             173 KSSYPGKITSNMFCLGFLEGGKDSCQGDSGGPVVCNGQLQGVVSWG-YGCAQKGKPGVYI 231
                                                                                                                                                                                                                                      142 KLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKEC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 KVCNFVGWIQDTIAAN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 KLSSPVKLNARVAPVALPSACAPAGTÇCLISGWGNTLSNGVNNPDLLQCVDAPVLSQADC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 KLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKEC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101;
                                                                                                                                                                                                                                                                                                  61 SAÄHCYKSRIQVRLGEHNIDVVEGGEQFIDAAKIIRHPSYN-----ANTFONDIMLI 112
                                                                                                                                                                                                                                                                                                                                                              83 TAAHCGNKPLWARVGDDHLLLLQ-GEQLERTTRSVVHPKYHQGSGPILPRRTDEHDLMLL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 LLMAQLWAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 TAAHCGNKPLWARVGDDHLLLLQG-EQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 LLWAQLWAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IJ
                                                                                                                                                                                                                                                                                                                                                                                                                     5 IFLAFLGAAVALPLODDDDKI---VGGYTCQKNSLPYQVSLNAGYHF-CGGSLINSQMVV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,9%; Score 477.5; DB 2; Length 247; Similarity 37.5%; Pred. No. 2.9e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                              EVFYPGVVTNNMICAG-LDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYT 260
                                                                                                                                                                     KLNSPATLNSRVSTVSLPRSCGSSGTKCLVSGWGNTLSSGTNYPSLLQCLDAPVLSDSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAAYPGEITSSMICVGFLEGGKDSCQGDSGGPVVCNGQLQGIVSWG-YGCALPDNPGVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAAHCYKSRIQVRLGEHNINVLEGDEQFINAAKIIKHPNYSSW-----TLNNDIMLI 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Gene 41, 305-310, 1986
A; Yitle Cloning, Characterization and nucleotide sequences of two cDNAs encoding huma
A, Beference number: A91544; MUID:86221712; PMID:3011602
A, Beference number: A91544; MUID:86221712; PMID:3011602
                                                                                                                                                                                                                                                                                        A;Cross-references; Gs:R47602, KD19521217, FIDN:AA861222.1, FID:9521218
R;Kinland, M.; Hussick, C.; Karks, W.H.; Borgstroem, A;
Clin, Chim. Acta 184, 31-46, 1989
A;Tilje: Immunosactive antionic and cationic trypsin in human serum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trypsin (8C 3.4.21.4) II precursor [validated] - human
N.Alernate names: trypsin 12; trypsin, anionic; trypsinogen II
C.Specise: Homo sapiens (man)
C.Specise: Ol-Mar.1994 flequence_revision Ol-Mar.1994 flext_change O8-Dec-2000
C.Jaccesion: B25852, A61066; B3398
R.Smi, M.; Nachmuta, Y.; Osawa, M.; Yamamoro, T.; Nishide, T.; Mori, T.; Mat
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                                                                                                                                                                                                                                                               A; Reference number: A61066; MUID: 90091010; PMID: 2598466
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-247 < EMI>
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A; Residues: 1-242 <GEN>
                                                                                                                                                                                                                                 A; Accession: A61066
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A)Cross-references: AMBL.882233 MID.955907, FIDN:CAA57701.1; FID:9559508
C:Superfamily: Lrypsin terypsin bendly-
C:Keypords: Mydrolass; serine proceinass
F:1-13/Domain: signal sequence Stratus predicted <81G>
F:1-13/Domain: signal sequence Stratus predicted <81G>
F:1-13/Product: trypsin Stratus predicted <8NT>
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submitted to the RMBL Data Library, October 1994
A.Description: Trypsin and trypsinogen from an antarctic fish: molecular basis of cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ryppin (8C 3.4.21.4) precureor - Paranotothenia magellanica
C.Specite: Paranotochenia magellanica
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C.Accession: 394499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;21-235/Domain: trypsin homology <TRY>
186 QGGKDSCQGDSGGPVVCNGELQGVVSNG-YGCAERDHPGVYAKVCLFNDWL 235
                                                                  219 DRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSWI 269
                                                                                                                                                                                                                                 160 YRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAG-L
                                                                                                                                                                                                                                                                                                                                                                                   101 LLLLQG-EQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVPGPRVRALQLP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 KVCNYVNWIQQTVAAN 247
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                                                                                                                                                                                                                                                                                                          75 IRVIEGKEGFISSSRVIRHPNYSS-----YNIDNDINLIKLSKPATLNQYVQAVALP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 TEEDKIVGGKBCSPYSQPHQVSLNSGYHF-CGGSLVNENWVVSAAHCYKSRVEVRMGEHH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 TRIDPEAYGAPCARGSQPWQVSIFNGLSFHCAGVIVDQSWVITAAHCGNKPLWARVGDDH 100
                                                                                                                                                        SSCAPAGIMCTVSGWGSTQSSSADGNK-LQCLNIPILSDRDCDNSYPGMITDAMPCAGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 473.5; DB 2;
Pred. No. 6.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                 218
                                                                                                                                                        185
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trygsin [8 d.3.4.21.4] II precursor, pancreatic (clone 2-P29) - chicken
NAlternate names: trypsinogen II
Cispecies (alius galius (chicken)
Cispecies (23-No-1995 #esemenc_revision 19-Oct-1995 #text_change 22-Jun-1999
Ciscossion, $55066; $72342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Superfamily, trypsin; trypsin homology
C.Kaynords: hydrolase; bancerss; protein digestion; serine proteinase; zymogen
F.1-15/Domain: signal sequence istatus preditted <SIOs
F.16-24/Froduct: trypsinogen II #status experimental <ZYM-
F.16-22/Jomain: activation peptide #status experimental <APT>
A, Böxpeifmentyl source; clone 2-2P3
C;Supycriamity, trypsin, trypsin homology
C;Supycriamity, trypsin, trypsin bomology
G;Keywords: Mydrolæer, pancress, procesn digestion; serine proteinase; zymogen
F)1-725/Domain: signal sequence flatus predicted <a href="https://domain.signal.sequence-flatus.predicted-dAF7">https://domain.signal.sequence-flatus.predicted-dAF7">https://domain.signal.sequence-flatus.predicted-dAF7">https://domain.signal.sequence-flatus.predicted-dAF7">https://domain.signal.sequence-flatus.predicted-dAF7</a>
F/26-241/Domain: trypsin homology <a href="https://domain.sequence-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-dafa-flatus.predicted-d
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A; Mote: the human genome contains at least ten trypsin genes or pseudogenes, at least tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: mucinous ovarian tumor cyst fluid C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 16-49 < KOI>
                                                                                                                                                                                                                                                                                                                                                   A.Polecule type: DNA
A.Polecule type: DNA
A.Poss-references: EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Crose-references: BMB1:UI$157, NID:g603906; PIDN:AAA79914.1; PID:g603907
A.Experimental source: Clome 2-P29
A.Experimental source: Clome 2-P29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K.Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A.Title: Implation and characterisation of the chicken trypsinogen gene family.
A.Reterence number: 585065; MUDI: 95251611; PMID: 77733885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
S55066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-248 < WAN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S55066
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Best Local S
Matches 99
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7:24-229/Domain: trypsin honology (7RY>
7:20-129/Domain: trypsin honology (7RY>
7:20-160, 48-64,171-185,196-220/Disulfide bonds: #status predicted
623,107,200/Active site: His, Asp. Ser #status predicted
7:5,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 KVYNYVDWIKDTIAAN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 TAAHCGNKPLWARVGDDHLLLLLQG-EQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 LLMNQLWAAEAALLFQNDTRLDFEAYGAFCARGSQFWQVSLFNGLSFHCAGVLVDQSWVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EASYPGKITNNMFCVGFLEGGKDSCQGDSGGPVVSNGELQGIVSWG-YGCAQKNRPGVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVFYPGVVTNNWICAG-LDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLSSPAVINSRVSAISLPTAPPAAGTESLISGWGNTLSSGADYPDELQCLDAPVLSQAEC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKEC
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Pred. No. 1.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 102; Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-238 <MAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M 8 0
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C;Species C;Date: 2 C;Accessi R;Male, R Eur. J. B A;Title: A;Referen A;Accessi	RESULT 15 S31779 trypsin (	Вb	Ş	Дb	γ	DD dd	8	문	Ś	В	φ	Matches	Query Match
C.Species: Salmo salar (Atlantic salmon) C.C.Species: Salmo salar (Atlantic salmon) C.Accession: S6657; 831779 R.Male, R.; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R. R.Male, R.; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R. A.Title: Molecular cloning and characterization of anionic and cationic variants of to A.Reference number: S6657; MUID:S603508; PMID:7556223 A.Reference number: S6657; MUID:S603508; PMID:7556223 A.Reference number: S6657; MUID:S603508; PMID:7556223	RESULT 15 331779 trypsin (BC 3.4.21.4) III precursor - Aclantic salmon (fragment)	229 GVYTKVCNYVDMIQETI 245	257 AVYTQICKYMSMINKVI 273	170 DQBCQEAYEGDITSNMICVGFLEGGKDSCQGDSGGPVVCNGELQGIVSMGI-GCALKGYP 228	z-rongopacospage	110 IMLIKLASAVEYSADIQPIALPSSCAKAGTECLISGWGNNTLSNGYNYPELLQCLNAPILS 169	138 IMLIKLARPVVPGBRVRALQLPVRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILS 197	58 QWVLSAAHCYKSRIQVRLGEYNIDVQEDSEVVRSSSVIIRHPKYSSITLNND 109	79 SWYLTAAHCGNKPLWARVGDDHLLLLQGEQLRRTTRSVV-HPKYHQGSGPILPRRTDEHD 137	2 KELFLILSCLGAAVAFPGGADDDKIVGGYTCPEHSVPYQVSLNSGYHF-CGGSLINS 57	19 KILPILMAQIMAAEAALIPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQ 78	Hest Local Similarity 38:58; Fied. No. 1.48-33; Matches 99; Conservative 52; Mismatches 91; Indels 15; Gaps 6;	

C.Superfamily: trypsin trypsin homology
C.Reywords hydrolase; sectine proceins #status predicted <816>
E1.E-1/Domain signal sequence (fragment) #status predicted <APT>
F18-15/Domain stypain month #status predicted <APT>
F18-15/Domain stypain III #status predicted <APT>
F16-28/Product: trypsin homol #status predicted <APT>
F16-28/Product: trypsin homol #status predicted <APT>
F16-28/Product: trypsin homol #status predicted <APT>
F16-28/Domain stypsin homol #status predicted f16-2-15/APTF16-28/Domain stypsin homol #status predicted complex f16-2-15/APTF16-28/Domain stypsin homol #s P,55,99,192/Active site: His, Asp, Ser #status predicted Matches Query Match Local Similarity 31 AEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNK 90 93; Conservative 31.3%; Score 468.5; DB 2; Length 238; 37.5%; Pred. No. 1.7e-33; 46; Pred. No. 1.7e-33; 5; Mismatches 94 Indels

172 231 269

TSNMFCAGFMEGGKDSCQGDSGGPVVCNGQLQGVVSWG-YGCAQRNKPGVYTKVCNYRSW TNIMICAG-LDRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSW 268

ISSTMSSN 238 INKVIRSN 276

171

4 ARAAPIDDEDDKI---VGGYECRKNSASYQASIQSGYHF-CGGSLISSTWVVSAAHCYKS 59

Search completed: November 25, 2003, 09:09:13 Job time : 28 secs

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1438.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1496
1496
1496
1496
                                    Published Applications An:

(SQRIZ 6) FOODSTATE // JOHDPAN/PCT NEW FUEL POP:

(SQRIZ 6) FOODSTATE // JOHDPAN/PCT NEW FUEL POP:

(SQRIZ 6) FOODSTATE // JOHDPAN/PCT NEW FUEL POP:

(SQRIZ 6) FOODSTATE // JOHDPAN/USOS 6_FUECOMS POP:

(SQRIZ 6) FOODSTATE // JOHDPAN/USOS 7_FUECOMS PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0
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1 MRAPHLHLSAASGARALAKL....AVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-021-368-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB ID
                             705-09-888-611-97
2 US-10-361-822-55
2 US-10-366-288-52
4 US-10-361-366-1
5 US-10-20-366-1

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1131.252 Million cell updates/sec
              Sequence 87, Appl
Sequence 52, Appl
Sequence 52, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 187, Appl
Sequence 184, App
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	45	44	3	42	41	6	39		37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7
	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248	248
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at townships	US-10-006-117A-194	-10-006-	US-10-012-121A-194	-10-015-869A-		US-10-006-818A-194			US-10-015-519A-194	US-10-015-394A-194	-10-013	US-10-015-389A-194	US-10-007-236A-194	US-10-015-385A-194	US-10-012-753A-194	US-10-015-715A-194	US-10-015-480A-194	US-10-015-388A-194	US-10-013-906A-194		US-10-015-671A-194	US-10-015-653A-194		-10-013-9127	US-10-013-911A-194	US-10-013-909A-194	US-10-012-754A-194	-10-012	012-137A-	US-10-012-101B-194
	Sequence 194,	194,	194,	194,	194,	194,	194,	194,	194,	194,	194,	194	194,	194,	194.	194,	194,	194,	194,	194,	194,	194,	194,	194,	194,	194,	194,	e 194.	194,	
	App	App	App	ddy	App	App	App	App	App	ddy	App	App	App	App	gqA	App	App	App	App	ddy	App	day	App Q	App	ddy	ddv	App	gga	App	App

#### ALIGNMENTS

US-09-888-615-87

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Sequence 87, Application US/0888615
Fatent No. US/0200206485614
GENERAL INFORMATION:
APPLICANT: PLOMMAN GEBOORY
APPLICANT: PLOMMAN GEBOORY
APPLICANT: CHANDEELS, SEAM
APPLICANT: WHYTE, DAVID
APPLICANT: CHANDEELS, SEAM
APPLICANT: WANNING, GEBOOR
APPLICANT: WANING, GEBOOR
APPLICANT: WANNING, G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-66-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PARENTIN Ver. 2.1
SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MANNING, GERARD
APPLICANT: SUDNARSAMAN, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 0366071281: US/09/888,615
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
121 YHQGSGPILPRRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAAR 180
                                                                                                                                                                                       61 VSLENGLSFHCAGVLVDOSWVLTAAHCGNKFLWARVGDDHLLLLQGEQLRRTTRSVVHFK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276; Conservative
                                                                                                                                                                                                                                                                                                                                                                              1 MRAPHIHISAASGARALAKIIPIIMAQIWAAEAALIPQNDTRIDPEAYGAPCARGSQPWQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRAPHIHISAASGARAIAKII,PILMAQIMAAEAAIIPQNDTRIDPEAYGAPCARGSQPWQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276
                                                                                                               VSLENGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQGBQLRRTTRSVVHPK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1496; DB 9; Length 276; 100.0%; Pred. No. 5.7e-141; ative 0; Mismatches 0; Indels 0
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REPLICANT: Will-contium pharmaceuticals, Inc.

APPLICANT: Milleonium pharmaceuticals, Inc.

APPLICANT: Berger, Allieon

APPLICANT: Berger, Allieon

APPLICANT: Camarter, Subhangi

APPLICANT: Monhan, John B.

TITLE OR TRUMFIGHT, MONGER DER DESTREET, KITS, AMD

TITLE OR TRUMFIGHT, MONGER DER DESTREET, MONGER DESTREET, MO
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RESULT 3
US-10-366-288-52
; Sequence 52, Application US/10366288
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US-10-301-822-95
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US-10-301-822-95
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Publication No. US20030148410A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              YHQGSGPILPRRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVKYNKGLTCSSITILSPKECEVPYPGVYTNAMICAGLDRQDPCQSDSGGPLVCDETLQ 240
RVKYNKGLTCSSITILSPKECEVPYPGVYTNAMICAGLDRQDDCQSDSGGPLVCDETLQ 240
RVKYNKGLTCSSITILSPKECEVFYPGVYTNAMICAGLDRQDDCQSDSGGPLVCDETLQ 240
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                                                                                                                                                                                                                                                                                  RVKYNKGLTCSSTTILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQ
                                                                                                                                                                                                                                                                                                                            RVKYNKGLTCSSITILSFKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                GILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                   YHQGSGPILERRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGMGTTAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQGEQLRRTTRSVVHPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1496; DB 12; Length 100.0%; Pred. No. 5.7e-141; Ative 0; Mismatches 0; Indels
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PEPLICANT: Dovell' Douglas

APPLICANT: MACINA MACINE S.

PEPLICANT: WESCA, MACINE S.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

TITLE OF INVENTION: ALDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1583,

TITLE OF INVENTION: ALDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1583,

TITLE OF INVENTION: ALDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1583,

TITLE OF INVENTION: ALDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1583,

TITLE OF INVENTION: 10002, 1611, 1391, 1434, 1262, 275, 312, 167, 326, 18926,

TITLE OF INVENTION: 10002, 1611, 1391, 1394, 1394, 1394, 1394,

TOTAL REPLICATION MARBER: 403, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1394, 1
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10021368 Publication No. US20020106367A1
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Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                               ADLICATION ...

APPLICANT: BAND, VALAGO POLYPEPTIDES, DNA, TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, TITLE OF INVENTION MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                 NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttch 100.0%; Score 1496; DB 12; Length 276; 21 Similarity 100.0%; Srod. No. 5.78-141; 276; Conservative 0; Mismacches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 RVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQ
STREET: 225 Franklin Street
CITY: Boston
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YHQSSGPILPRRIDEHDLMLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAAR 180
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                                                                                                        ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                               AND RELATED
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// SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-021-368-1
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US-10-097-340-167
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Best Local Similarity
                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                            Sequence 167, Application US/10097340 Publication No. US20030087250A1
                                                                                                                                                                 APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT:
                                          APPLICANT:
                                                               APPLICANT:
                                                                                APPLICANT:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
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ATTOSNEY/GERF INFORMATION:
NAME: Clark, Paul T.
REGISTRATON UNDER: 00.162
REGISTRATON UNDER: 00.162
REFERENCE/COCKET WUNER: 00389/100002
TELEPHONE: 617/842-8070
TELEPHONE: 617/842-8070
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FILING DATE: 12-Dec-2001
CLASSIFICATION: «URKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER: FIORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN NATA-
CURRENT APPLICATION DATA-
CURRENT APPLICATION DATA-
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                                      Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVANS
Rachel E. MEYERS
Michael MORRISBY
Peter OLANDT
Ami SEN
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Peter VEIBY
Gordon B. MILLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1496; DB 14; Length 276; 100.0%; Pred. No. 5.7e-141;
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TITLE DE INVENTION NUCLEIC Acid Molecules and Procesins For The Identification, ITILE DE INVENTION Assessment, Prevention, and Therapy of Overian Cancer CURRENT APPLICATION MUNBER: US/10/097,340

CURRENT APPLICATION MUNBER: US/20/097,340

CURRENT FILING DATE: 2002-03-14

FEIOR APPLICATION MUNBER: 60/276,025

FEIOR APPLICATION MUNBER: 60/276,026

FEIOR APPLICATION MUNBER: 60/235,102

FEIOR APPLICATION MUNBER: 60/233,500

MUNBER OF SEO ID NOS. 153

SOFTWARE: FRANCE 2001-09-19

MUNBER OF SEO ID NOS. 153

SOFTWARE: FRANCE 2001-09-19

MUNBER OF SEO ID NOS. 153

SOFTWARE: FRANCE 2001-09-19

MUNBER OF SEO ID NOS. 153

SOFTWARE: FRANCE 2001-09-19

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SOFTWARE: FRANCE 2001-09-19

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SOFTWARE: FRANCE 2001-09-19

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SOFTWARE: FRANCE 2001-09-19

MUNBER OF SEO ID NOS. 153

SOFTWARE: FRANCE 2001-09-19

MUNBER OF SEO ID NOS. 153
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Band, Vimla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VSLENGLSPHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQGBQLRRTTRSVVHPK 120
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert C. BAST, Jr.
Karen LU
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                                                                                                                                                                                                                                                                       MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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RESULT 7
US-09-946-374-194
US-09-946-374-194
; Sequence 194, Application US/09946374
; Publication No. US20030073129A1
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Best Local Sin
Matches 276;
                                                                                                                                                                                                                                                  GENERAL
                                                                                                                                                  APPLICANT:
                                                                                                                                                                                     APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                            APPLICANT:
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                               APPLICANT
                                                   APPLICANT
                                                                      APPLICANT:
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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OPERATING SEVERH PC COMPARISH:

SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APELICATION NAMA:

APPLICATION WHOSER: US/10/31/368
FILING MUSIC: 12-Dec-2001
PRIOS APPLICATION DATA:

PRIOS APPLICATION DATA:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100002
TELECOMMUNICATION INFORMATION:
TELERHOME: 61,7/442-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/201,038
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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Fong, Sherman
Gao, Rei-Oiang
Goddard, Audrey
Goddwski, Paul J
Grimaldi, Christopher J.
Gurney, Austin L
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                           SGGPLVCDETLQGILSWGVYNESPCGSAQHPAVYTQICKYMSWINKVIRSN 291
                                                                                                                                                                                                                                                                                                                                                                                                                        SGGPLVCDETLQGILSWGVY----PCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGWGTTAARRVKYNKGLTCSSITILSPK---ECEVFYPGVVTNNMICAGLDRGQDPCQSD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVP---GPRVRALQLPYRCAQPGDQCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDH----LLLLQGEQLRRTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRAPHLHLSAASGARALAKLLPILMAQLWAAEAALLEQNDTRLDPEAYGA---PCARGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGWGTTAARRVKYNKGLTCSSITILSPKNBSBCEVFYPGVVTNNMICAGLDRGQDPCQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVPNESGPRVRALQLPYRCAQPGDQCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHNESLLLLQGEQLRRTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                  Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617/542-8906
                                                                                                                                               Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.2%;
ilarity 94.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1438.5; DB 14; Length 291;
Pred. No. 3.3e-135;
0; Mismatches 0; Indels 15;
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PRIOR FILTNG DATE: 1998-09-01
PRIOR RELITNG DATE: 1998-09-02
PRIOR RELITNG DATE: 1998-09-02
PRIOR RELITNG DATE: 1998-09-02
PRIOR RELITNG DATE: 1998-09-02
PRIOR PELLING DATE: 1998-09-02
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CURRENT FILING DATE: 2007-09-04
PRICOR APPLICATION NUMBER: 60/098716
PRICOR PELIZE DATE: 1998-00-01
PRICOR APPLICATION NUMBER: 60/098723
PRICOR APPLICATION NUMBER: 60/098749
PRICOR APPLICATION NUMBER: 60/098749
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APPLICANT: Mod. Milliam I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILS REPERENCE: P8830PLC1
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                            DE APELICATION NUMBER: 60/100662
DE PILINO DATE: 1998.09-1
DE APPLICATION NUMBER: 60/100664
DE PILINO DATE: 1998-09-16
DE APPLICATION NUMBER: 60/100683
DE APPLICATION NUMBER: 60/100684
DE APPLICATION NUMBER: 60/100684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NA PELLANTON NUMBER: 60/09972
NE TILING NATE: 1998-09-10
NA PELLANTON NUMBER: 60/09988
NA PELLANTON NUMBER: 60/099882
NA PELLANTON NUMBER: 60/099812
NA PELLANG NATE: 1998-09-10
NATE OF PELLANG NATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NR APPLICATION NUMBER: 60/09816
NR FILING DATE: 1998-09-10
NR APPLICATION NUMBER: 60/100385
NR FILING DATE: 1998-09-15
NR APPLICATION NUMBER: 60/100386
NR FILING DATE: 1998-09-15
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/100584
FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100627
FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100661
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                                                                                                                                                                                                                                                                                          FILING DATE: 1998-09-16
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FILING DATE: 1998-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/099754
FILING DATE: 1998-09-10
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Tumas, Daniel
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1998-09-17
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PRIOR EPELICATION NIMER: 60/100711
PRIOR ELIKER DATE: 1938-9-17
PRIOR APPLICATION NUMBER: 60/100848
PRIOR PRILING DATE: 1938-90-18
PRIOR PRILING DATE: 1938-90-17
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PRIOR APPLICATION NUMBER: 60/101475
PRIOR PILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101476
PRIOR PILING DATE: 1998-09-23
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PRIOR FILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-18
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NR FILING DATE: 1998-09-29
DR: APPLICATION NUMBER: 60/102307
DR FILING DATE: 1998-09-29
DR APPLICATION NUMBER: 60/102330
DR FILING DATE: 1998-09-29
DR FILING DATE: 1998-09-29
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DE APELICATION UNUBER: 60/101915

DE FILING DATE: 1998-09-24

DE APELICATION UNUBER: 60/101916

DE APELICATION WHERE: 60/10207

DE FILING DATE: 1998-09-24

DE FILING DATE: 1998-09-24

DE FILING DATE: 1998-09-24
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APPLICATION NUMBER: 60/101471
FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101472
FILING DATE: 1998-09-23
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FILING DATE: 1998-09-30
APPLICATION NUMBER: 60/102487
FILING DATE: 1998-09-30
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FILING DATE: 1998-09-29
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FILING DATE: 1998-09-24
APPLICATION NUMBER: 60/101743
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FILING DATE: 1998-09-24
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FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101479
FILING DATE: 1998-09-23
                     APPLICATION NUMBER: 60/103314
FILING DATE: 1998-10-07
                                                                        FILING DATE: 1998-10-06
                                                                                              FILING DATE: 1998-10-02
APPLICATION NUMBER: 60/103258
                                                                                                                                                 APPLICATION NUMBER: 60/102965
                                                                                                                                                                               APPLICATION NUMBER: 60/102687
FILING DATE: 1998-10-01
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FILING DATE: 1998-09-30
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FILING DATE: 1998-09-17
NUMBER: 60/103315
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PRIOR APPLICATION NUMBER: 60/103328
PRIOR RILING DATE: 1998-10-07
PRIOR RILING DATE: 1998-10-07
PRIOR PRIOR
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Best Local
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PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NÜMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
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                                                                      260
                                                                                                                                                         172 CHGYYPGRITSWWYCAGGYPGQDACQGDSGGPLYCGGYLQGLYSWGSYGPCGQDGIPGYY
                                                                                                                                                                                                                                                                                                                   112
232 TYICKYVDWIRMINRNN 248
                                                                                                                                                                                                                               201 CEALABOALINMICYCTDECOPEOSOSCEPTACOELTOCITYMC-ALECCENOHDAAA
                                                                                                                                                                                                                                                                                                                                                                      141 LKLARPVVPGPRVRALQLEVRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 LTAAHCSGSRYWVRLGEHSLSQLDWTBQIRHSGFSVTHPGYLGAS-----TSHEHDLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 LTAAHCGNKPLWARVGDDHLLLLQ-GEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 LLMAQLMAAEAALLPQNDTRLDPEAY-GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LLCVLGLSQAA-----TPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                               TOICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                   LREALPYRVISSYOPEPEPNDCATAGTECHVSGWGITNHPRNPFPDLEQCENLSIVSHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.7%; Score 564; DB 11; 1
45.9%; Pred. No. 4.8e-48;
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Gaps

171 111 140

REGUTA 9
US - 10-015-397A-194
J. Sequence 194, Application US/10015387A
J. Sequence 194, Application US/10015304A1
J. SCHERAL THROMONICON:
APPLICANT: Before Kevin P.
APPLICANT: Before Servin David
APPLICANT: Before Servin Company Company Company Device Nac.
APPLICANT: Before Device Nac.

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US-10-006-130A-194
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CIREBET PILLO ADTE: 2001-12-12
PRIOR POLYPE APPLICATION NUMBER: UB/10/015,387A
UNNESSY PILLO ADTE: 300-12-12
NUMBER OF SGI DI NOS: 477
NUMBER OF SGI DI NOS: 477
BERTI: 248
BERTI: 248
                    APPLICANT: Rong, Shermin
APPLICANT: Goddard, Andrey
APPLICANT: Goddard, Andrey
APPLICANT: Goddard, Andrey
APPLICANT: Goddard, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hallan, James
APPLICANT: Baoni, Nicholas F.
APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 194, Application US/10006130A Publication No. US20030148375A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
Prior Application removed - See File Wrapper or Palm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 TYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 CEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWG-VYPCGSAQHPAVY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 LKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 LLMAQLWAAEAALLPQNDTRLDPEAY-GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWV
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Gao, Wei-Qiang
Goddard, Audrey
Goddweki, Paul J
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHGVÝPGRITSNMVCÁGGVPGQDÁCQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVÝ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRLRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHAT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTAAHCGNKPLWARVGDDHLLLLQ-GEQLERTTRSVVHPKYHQGSGPILPRRTDEHDLML 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eaton, Dan 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 248;
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, NUMBER OF SEQ ID NOS: 477
SEQ ID NO 194
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
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REIOR FILING MATE: 1998-09-01

REIOR FILING MUNER: 500,09150

REIOR FILING MUNER: 500,09150

REIOR FILING MUNER: 500,098803

REIOR FILING MUNER: 500,002

REIOR FILING MUNER: 500,002
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APPLICANT: Annes P.
APPLICANT: Annes, Nicholas F.
APPLICANT: Annes, Nicholas F.
APPLICANT: Annes, Nicholas F.
APPLICANT: Annes, Nicholas F.
APPLICANT: Annes Polypeptides and Nucleic
TITLE OF INVESTIGN SPACES PROOFING
THE ANNES PROPERTY OF ANNES PROPERTY AND PROPERTY ANNES PROPERTY AND PROPERT
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             PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR TILING DATE: 1998-09-09
PRIOR TILING DATE: 1998-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
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APPLICATION NUMBER: 60/099596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 TYICKYVDWIRMIMRNN 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 CHGVYPGRITSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 LKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKE 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, Christopher J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLCVLGLSQAA-----TPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/10006172A
o. US20030153000A1
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PRIOR RIOR RIOR IN PILLING DATE: 1998-09-18

REPLICATION MUNERE: 60/10/279

REPLING DATE: 1998-09-22

REPLING DATE: 1998-09-22

REPLING DATE: 1998-09-23

REPLING DATE: 1998-09-23

REPLING DATE: 1998-09-23

REPLING DATE: 1998-09-23

REPLING DATE: 1998-09-23 NE FILING DATE: 1998-09-17

BR APELICATION WINNER: 60/100930

ME FILING DATE: 1998-09-17

DR APELICATION WINNER: 60/101014

R FILING DATE: 1998-09-18

ME FILING DATE: 1998-09-18

ME FILING DATE: 1998-09-18

ME FILING DATE: 1998-09-18 R APELICATION NUMBER, 60/100388
R FILING DATE: 1998-09-15
R APPLICATION NUMBER: 60/100390
R FILING DATE: 1998-09-15
R R FILING DATE: 1998-09-16
R FILING DATE: 1998-09-16
R FILING DATE: 1998-09-16 FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099812
APPLICATION 1998-09-10
FILING DATE: 1998-09-20 APPLICATION NUMBER: 60/101475 FILING DATE: 1998-09-23 APPLICATION NUMBER: 60/101476 FILING DATE: 1998-09-23 APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/100849
FILING DATE: 1998-09-18 APPLICATION NUMBER: 60/100710 FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/100711 APPLICATION NUMBER: 60/100683 FILING DATE: 1998-09-17 APPLICATION NUMBER: 60/100684 FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100664
FILING DATE: 1998-09-16 APPLICATION NUMBER: 60/100385 FILING DATE: 1998-09-15 APPLICATION NUMBER: 60/099815 APPLICATION NUMBER: 60/0 FILING DATE: 1998-09-10 APPLICATION NUMBER: 60/099754 FILING DATE: 1998-09-10 APPLICATION NUMBER: 60/099598 APPLICATION NUMBER: 60/100919 FILING DATE: 1998-09-17 FILING DATE: 1998-09-16 APPLICATION NUMBER: 60/100662 APPLICATION NUMBER: 60/100663 APPLICATION NUMBER: 60/100627 APPLICATION NUMBER: 60/099816 APPLICATION APPLICATION FILING DATE: 1998-09-APPLICATION NUMBER: 60/09974: APPLICATION NUMBER: 60/099642 APPLICATION NUMBER: 60/099602 FILING DATE: 1998-09-09 FILING DATE: 1998-09-FILING DATE: FILING DATE: FILING DATE: 1998-09-10 FILING DATE: 1998-09-09 LING DATE ING DATE: 1998-09-09 NUMBER: 60/099808 1998-09-10 NUMBER: 60/099792 NUMBER: 60/099763 1998-09-16 1998-09-10

PRIOR REPLICATION HUMBER: 60/10447

PRIOR PLICATION HUMBER: 60/10147

RETIOR PLILING DATE: 1996-90-23

RETIOR PLILING DATE: 1996-90-24

PRIOR PLILING DATE: 1996-90-29

PRIOR PLILING DATE: 1996-90-30

PRIOR PLILING DATE: 1996-90-30

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PRIOR PLILING DATE: 1996-90-30

PRIOR PLILING DATE: 1996-00-30

PRIOR PLILING DATE: 1996-10-06

PRIOR PLILING DATE: 1996-10-07

PRIOR PLILING DATE: 19

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APPLICANT: Pann, Mames

APPLICANT: Panni, Micholas P.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: PRESUPCING MUNISER: UB/10/015,392A

PURKENT PILLNG DATE: 1939-1950-1971

PRIOR PILLNG LOWE: 1939-19-10 198716

PRIOR PILLNG LOWE: 1939-09-01

PRIOR PILLNG MATE: 1939-09-01
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US-10-015-392A-194
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Best Local Similarity 45.9
Matches 118; Conservative
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OR APPLICATION MUNERE: 60/10266

OR APPLICATION MUNERE: 60/102693

OR APPLICATION MUNERE: 60/106593

OR PILING DATE: 1998-10-26

OR PILING DATE: 1998-10-26

OR PILING DATE: 1998-10-27

OR PILING DATE: 1998-10-28

OR PILING DAT
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FILING DATE: 1998-10-27
APPLICATION NUMBER: 60/106023
FILING DATE: 1998-10-28
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Gao, Wei-Qiang
Goddard, Audrey
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Pred. No. 4.8e-48;
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APPLICANT: APPLICANT:

Botstein, David Desnoyers, Luc Eaton, Dan 1.

APPLICANT: Baker, Kevin P.

INFORMATION:

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

> Goddard, Audrey Ferrara, Napoleone Fong, Sherman Gao, Wei-Qiang

APPLICANT: APPLICANT:

Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, Jemes
Pan, Jemes
Pandi, Nicholas F.

APPLICANT:

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Films per INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Films Repeated: Page 1000 Acids Encoding the Same Films Repeated: Page 1000 Acids Encoding the Same Films Page 1000 Acids Inventor Invent

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Best Local Similarity 45.9%;
Sequence 194, Application US/10017253A Publication No. US20030166055A1
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                                                                                                            260 TQICKYMSWINKVIRSN 276
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Pred. No. 4.8e-48;
29; Mismatches 92
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RESULT 13
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NUMMEER OF EGO ID NOS: 477
SEQ ID NO 194
LENGTH: 248
LENGTH: 248
TYPE: PPT
TYPE: PPT
COMPANIENT: FORM Captions
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
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Best Local Similarity
         APPICANT: Pool, Nicholas F.
TITHE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic PILE PILE PROPERTION: Acids Encoding the Same
FILE REFERENCE REPROPERTY APPLICATION NUMBER: US/10/017,306A
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CURRENT FILING DATE:
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APPLICATION NUMBER: 60/099536
FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099596
FILING DATE: 1998-09-09
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FILING DATE: 1998-09-02
APPLICATION NUMBER: 60/098843
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FILING DATE: 1998-09-01
APPLICATION NUMBER: 60/098803
FILING DATE: 1998-09-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 37.7%; Score 564; DB 12; Length 248; al Similarity 45.9%; Pred. No. 4.88-48; Indels 118; Conservative 29; Mismatches 92; Indels 1
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                                                                                                                                     Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Fong, Sherman
Gao, Wei-Qiang
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Eaton, Dan 1.
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2002-06-10
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CTREENT ADDICONTON NUMBER: US/10/012,064A
CURRENT PLING DATE: 10920/0120-15
PRIOR PAPALICATION NUMBER: 00/0997.6
PRIOR PLING DATE: 1099-09-01
PRIOR PLING DATE: 1099-09-01
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PRIOR PRIOR DATE: 1099-09-01
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PRIOR PLING DATE: 1099-09-02
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; ORGANISM: Homo sapiens
US-10-017-306A-194
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NUMBER OF SEQ ID NOS: 477
SEQ ID NO 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: P2830P1C19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TQICKYMSWINKVIRSN 276
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Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth J.
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Pred. No. 4.8e-48;
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RESULT 15
US-10-017-867A-194
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                                      FILE REFERENCE: P9830F15C60

CURRENT PELLOW DATE: 2001-12-13

PRIOR APPLICATION NUMBER: US/20/07/867A

PRIOR PILLOW DATE: 2001-12-13

PRIOR PILLOW DATE: 1998-09-01

PRIOR PILLOW DATE: 1998-09-01
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LENGTH: 248
TYPE: PRT
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PRIOR PELIKE UNTE: 1998-9-09
PRIOR APELICATION NUMBER, 60/099598
PRIOR PELIKE TITUS UNTE: 1998-9-09
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: 60/098821
FILING DATE: 1998-09-02
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Fong, Sherman
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Desnoyers, Luc
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PRIOR ETILIO DATE: 198-09-10

OR PELINGTON MINERE: 60/10/99746

OR APPLICATION MINERE: 69-10

OR FILING DATE: 198-09-10

OR FILING DATE: 198-09-10

OR PELING DATE OR PILING DATE: 1998-09-18
OR APPLICATION NUMBER: 6/1/00919
OR APPLICATION NUMBER: 6/1/00919
OR APPLICATION NUMBER: 6/1/100919
OR APPLICATION NUMBER: 6/1/101014
OR FILING DATE: 1998-09-17
OR APPLICATION NUMBER: 6/1/10106
OR FILING DATE: 1998-09-18
OR APPLICATION NUMBER: 6/1/101071
OR FILING DATE: 1998-09-18
OR APPLICATION NUMBER: 6/1/101279
OR FILING DATE: 1998-09-18
OR APPLICATION NUMBER: 6/1/101279
OR FILING DATE: 1998-09-19
OR FILING DATE: 1998-09-19
OR APPLICATION NUMBER: 6/1/101471
OR FILING DATE: 1998-09-19 RE FILING DATE: 1998-09-17
PR PRILING DATE: 1998-09-17
PR FILING DATE: 1998-09-17
PR APPLICATION WUNBER: 60/100848
PR FILING DATE: 1998-09-18
PR APPLICATION WUNBER: 60/100849 IN ADDILIOTION NUMBER: 60/100662
IN FILING BARE. 1986-09-16
IN FILING BARE. 1986-09-16
IN FILING BARE. 1986-09-16
IN ADDILIOTION NUMBER: 60/100683
IN FILING BARE. 1986-09-17
IN ADDILIOTION NUMBER: 60/100684
IN FILING BARE. NUMBER: 60/100710 APPLICATION NUMBER: 60/098843 FILING DATE: 1998-09-02 APPLICATION NUMBER: 60/099536 FILING DATE: 1998-09-09 APPLICATION NUMBER: 60/099642
APPLICATION NUMBER: 60/099642
APPLICATION NUMBER: 60/099741 APPLICATION NUMBER: 60/099602 APPLICATION NUMBER: 60/099598 FILING DATE: 1998-09-09 APPLICATION NUMBER: 60/099596

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PRIOR PETLIZATION NUMBER: 60/102497
PRIOR PETLIZA DATE: 1398-09-30
PRIOR PETLIZA DATE: 1398-09-30
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OR FILING DATE: 1998-09-24
OR RAPPLICATION NUMBER: 60/101741
OR FILING DATE: 1998-09-24
OR RAPPLICATION NUMBER: 60/101743
OR FILING DATE: 1998-09-24
OR FILING DATE: 1998-09-24
OR RAPPLICATION NUMBER: 60/101915
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FILING DATE: 1998-09-23
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APPLICATION NUMBER: 60/101475
FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101476
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Best Local Similarity 45.9%; Pred, No. 4.8e-48;
Matches 118; Conservative 29; Mismatches 92; Indels
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BR PILLED INTE: 1998-10-26
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BR PILLED INTE: 1998-10-27
BR PILLED INTE: 1998-10-29
BR PILLED INTE: 1998-
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DE PILING DATE: 1998-10-20
DE PILING DATE: 1998-10-20
DE PILING DATE: 1998-10-21
DE PILING DATE: 1998-10-21
DE PILING DATE: 1998-10-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 LKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 LTAAHCGNKPLWARVGDDHLLLLQ-GEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 LLMAQLWAAEAALLPQNDTRLDPEAY-GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWV
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TYICKYVDWIRMIMRNN 248
                                                                                                                                                                TOICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                    CHGVYPGRITSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVY
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18; Gaps

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Search completed: November 25, 2003, 09:13:57 Job time: 48 secs

OM protein - protein search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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November 25, 2003, 09:06:20; Search time 22:Seconds (without alignments) 530.809 willion cell updates/sec
Sequence 1, Appli
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sequence 19, Appli
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US-08-467-155A-1
                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: not relevant
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Patent No. 573677
GENERAL INFORMATION:
APPLICANT: BAND, VIALA
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA,
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA,
                                                                                                                                        Query Match
Best Local Similarity
Matches 276; Conserv
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COMPUTER READALE FORM:

WEDIUM TYPE: Floppy disk

WEDIUM TYPE: Floppy disk

CONSUTER IM PC-COS/NS-DOS

ONERATING SYSTEM: PC-COS/NS-DOS

ONERATING SYSTEM: PC-COS/NS-DOS

ONERATING SYSTEM: PC-COS/NS-DOS

ONERATING SYSTEM: PC-COS/NS-DOS

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REGISTRATION UNDERS: 03.162

REGISTRATION UNDERS: 03.162

REGISTRATION UNDERS: 03.163

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CORRESCONDENCE ADDRESSE:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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CITY: Boston
STATE: MA
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US-08-478-195-9
US-08-472-187-9
US-08-472-187-9
US-08-472-187-9
US-08-472-187-9
US-08-472-187-9
US-08-181-9
US-08-181-99
US-09-074-689-9
US-09-106-466-9
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                                                                                                                                        Score 1496; DB 1;
Pred. No. 3.4e-146;
D; Mismatches 0;
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Result No.

Query Match Length DB

ij

Description

US-08-467-155A-1 US-08-628-198-1 US-09-201-038-1

1496 1496 1438.5 1438.5 1438.5 1438.5

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

I saud patente A1.\*

1 /cgn2 6/pcodata/2/iaa/5A COMB.pep:\*
2 /cgn2 6/pcodata/2/iaa/5B COMB.pep:\*
3 /cgn2 6/pcodata/2/iaa/6A COMB.pep:\*
4 /cgn2 6/pcodata/2/iaa/6A COMB.pep:\*
5 /cgn2 6/pcodata/2/iaa/6B COMB.pep:\*
6 /cgn2 6/pcodata/2/iaa/bacctflasi.pep:\*

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Recht 1986 1934 31 185 41 185

522.5 522.5 522.5 513 507.5 503.5

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Database

Post-processing: Minimum Match 0%
Maximum Match 10 Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries

Total number of hits satisfying chosen parameters:

328717

328717 segs, 42310858 residues Gapop 10.0 , Gapext 0

Searched: Scoring table: Sequence: Title: Perfect score:

BLOSUM62

1496 US-10-021-368-1

MRAPHLHLSAASGARALAKL....

....AVYTQICKYMSWINKVIRSN 276

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                                                                                                                                                                                                                                                                         INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acida
TYPE: amino acid
STRANDEDNESS: not relevant
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ZIF: 02110-2804

COMPUTER EXABAGE FORM:
MEDIUM TYPE: #loppy disk
MEDIUM TYPE: #loppy disk
COMPUTER: ISM PC COMPUTER: PO-TOS/MS-DOS
SOFTWARE: DATE-DE FELONION DATA:
SOFTWARE: DATE-DATA: PO-TOS/MS-DOS
OUREENT APPLICATION DATA:
APPLICATION NUMBER: 08/05/05.155
APPLICATION NUMBER: 08/05/05.155
APPLICATION NUMBER: 08/05/05.155
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Patent No. 5843694
                                                                                                                                             Matches 276;
                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                   REPLICANT: BAND, VIMLA
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fash & RICHARDSON P.C.
                                                                                                                                                                                                                                         MOLECULE TYPE:
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CITY: Boston
STATE: MA
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                                                                                                                                                                  Similarity
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VS_PROLSFICAGVIADOSWILTBANGCORKEDMARVODDHLLIAGGEOLBRITESVVHEK 120
VS_PROLSFICAGVIADOSWILTBANGCORKELMARVODDHLLIALGGEOLBRITESVHEK 120
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                                                                                                          MRAPHLHISAASGARALAKILPIIMAQIMAAEAALIPQNDTRIDPBAYGAPCARGSQPWQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08628198
VSLFNGLSFHCAGVLVDQSWVLTAAHCGNKFLWARVGDDHLLLLQGBQLRRTTRSVVHPK 120
                    VSLENGISFHCAGVIVDQSWVIJAAHCGNKPLWARVGDDHLILLQGEQLRRTTRSVVHPK 120
                                                                      MRAPHIHISAASGARALAKLIPILMAQUWAAEAALIPQNDTRLDPEAYGAPCARGSQPWQ 60
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                                                                                                                                                Conservative
                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                            not relevant
                                                                                                                                                               100.0%; Score 1496; DB 2;
100.0%; Pred. No. 3.4e-146;
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                                                                                                                                                Mismatches
                                                                                                                                                   0
                                                                                                                                                                                    Length 276;
                                                                                                                                                   Indels
                                                                                                                                                   0;
                                                                                                                                                   Gaps
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TYPE: amino acid
STRANDENNESS: not
TOPOLOGY: linear
MOLECULE TYPE: prot
US-09-201-038-1
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Best Local (
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APPLICANT: BAND, YIM1A
ITTLE OF INVENTION: NES-LIPOLYPEPTIDES, DI
ITTLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES. 1
                                                                                                                                                                                                                                                                                                                                                                       Matches
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Flooppy dak
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARS: PS desentin Selesse #1.0, V
CURRENT APPLICATION DATA:
APPLICATION MOMBER: US/SO/201,038
PRICA REPLICATION DATA:
APPLICA REPLICATION DATA:
PRICA REPLICATION DATA:

PRICA REPLICATION DATA:

OFFICE APPLICATION DATA:

OFFICE 
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T.
NAME: CLARK, PAUL T.
REGERRENCY-DOCKET NUMBER: 0019
TELECOMMUNICATION, INFORMATION:
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STATE: MA
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TELEFAX: 617/542-8906
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121 YHQGGGPILFRRIDEHDLMLLKLARPVVFGFRVRALQLFYRCAQFGDQCQVAGWGTTAAR
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                                                                                                                                                                                                                                                                                                                                                        n 100.0%; Score 1496; DB 3;
Similarity 100.0%; Pred. No. 3.4e-146;
76; Conservative 0; Mismatches 0:
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VSLENGLSEHCAGUUVQSWULTAANGGAKELMARVOODHLLLAGGEGLBRTTREVUHEK 120
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Best Local Similarity
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NAME: Clark, Paul T.
REGISTRATION UNDER: 30,162
REFERENCE/DOCKET NUMBER: 0035
TELECOMMUNICATION: TROPOMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
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MEDIUM TYRE: Floppy disk
COMPUTER: ITBM PC Compatible
OPERATING 9872EM: PC-DOS/MS-DOS
SOPTMARE: PALENTIN BATA:
CHREMET APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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PRIOR APPLICATION DATA,
APPLICATION NUMBER: 08/467,155
FILING DATE: 06-JUN-1995
CLASSIFICATION:
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STRANDEDNESS: not
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CITY: Boston
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STREET: 225 Franklin Street
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     RVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQ 240
                                                                                                                 VSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLMARVGDDHLLLLQGBQLRRTTRSVVHPK 120
                                                                       YHQGSGPILPRRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAAR 180
                                         YHQGSGPILPRRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAAR 180
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Pred. No. 3.4e-146;
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OPERATING SUSTEM: DC-DOG/MS-DOS
OPERATING SUSTEM: DC-DOG/MS-DOS
SOSTWARES: Batentin Release #1.0, Ves
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/467,185A
FILING DATE: 06-UNH-1995
CLASSIFICATION: 415
CLASSIFICATION: 415
CLASSIFICATION: 415
CRESTENATION WINDER: 30.162
REGISTRATION MINDER: 30.162
REGISTRATION LINDOMATION:
TRECEMBER: 1, 21, 24, 24, 24, 20, 00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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TITLE OF INVENTION: MES-1 POLYPEPTIDES, DNA,
TITLE OF INVENTION: WOLECULES AND METHODS
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Local Similarity 94.8%;
hes 276; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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TELEX: 200154
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                                                                                                                                                  121 SVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVPNESGPRVRALQLPYRCAQPGDQCQV
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SGGPLVCDETLOGILSWGVYNESPCGSAOHPAVYTQICKYMSWINKVIRSN 291
                          SGGPLVCDETLQGILSWGVY----PCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                          AGWGTTAARRVKYNKGLTCSSITILSPKNESECEVFYPGVVINNMICAGLDRGQDPCQSD
                                                                                                  AGWGTTAARRVKYNKGLTCSSITILSPK----BCEVFYPGVVTNNMICAGLDRGQDPCQSD 228
                                                                                                                                                                                     SVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVP---GPRVRALQLPYRCAQPGDQCQV 171
                                                                                                                                                                                                                         PWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHNESLLLLQGEQLRRTTR
                                                                                                                                                                                                                                                                                                    MRAPHIHLSAASGARALAKILPILMAQUWAAEAAILPQNDTRIDPEAYGANESPCARGSQ 60
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Best Local Similarity
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Patent No. 5843694
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APPLICANT: Band, Vimla
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INFORMATION FOR SEQ ID NO: 11:
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ANTONENEY/AGENT INFORMATION:
REGISTRATION NUMBER: 00199/100002
REGISTRATION NUMBER: 00199/100002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED TITLE OF INVENTION: WOLSCULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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CITY: Boston
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SGGPLVCDETLQGILSWGVYNESPCGSAQHPAVYTQICKYMSWINKVIRSN 291
                                                                                                                                                   SVYHEKYHOGSGFILERRTDEHDLMLLKLAREVVENESGERVRALQLEYRCAQEGDQCQV 180
                                                                                                                                                                        SVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVP----GPRVRALQLPYRCAQPGDQCQV 171
                     SGGPTACDETTOGITSMGAY---- BCGSAQHBAVYTQICKYMSMINKVIRSN 276
                                                                           AGWGTTAARRVKYNKGLTCSSITILSPKNESECEVFYPGVVTNNMICAGLDRGQDPCQSD 240
                                                                                                            AGWGTTAARRVKYNKGLTCSSITILSPK---ECEVFYPGVVTNNMICAGLDRGQDPCQSD 228
                                                                                                                                                                                                                              PWQVSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHNESLLLLQGEQLRRTTR 120
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Pred. No. 3.1e-140;
0; Mismatches 0;
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RESULT 7

RESULT 8
PCT-US96-07343-11
Sequence 11, Application PC/TUS9607343
GENERAL INFORMATION:

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Patent No. 6153387
GENERAL INFORMATION:
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYRE: Floppy disk
COMPUTER: IRM For Compatible
OPERATING WIZTEN: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
UURSENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BANG, VANIA
TITLE OF INVENTION: MISS-1 POLYPEPTIDES, DNA,
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBERS OF SECRETICES: 11
ADDRESSEE: Figh & Richardson P.C.
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TOPOLOGY: linear
MOLECULE TYPE: protein
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
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APPLICATION NUMBER:
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CITY: Boston
STATE: MA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 291 amino acids
TYPE: amino acid
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SGGPLVCDETLQGILSWGVYNESPCGSAQHPAVYTQICKYMSWINKVIRSN
                       SGGPLVCDETLQGILSWGVY---PCGSAQHPAVYTQICKYMSWINKVIRSN
                                                                         AGWGTTAARRVKYNKGLTCSSITILSPKNESECEVFYPGVVTNNMICAGLDRGQDPCQSD
                                                                                                         AGWGTTAARRVKYNKGLTCSSITILSPK---ECEVFYPGVYTNNMICAGLDRGQDPCQSD
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Pred. No. 3.1e-140;
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RESULT 9
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                              Sequence 2, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
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Best Local S
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0039
TELECOMPUNICATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acid
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MEDIUM TYEES, Floopy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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TITLE OF INVENTION: NES-I POLYEPTIED NA, AND RELATED
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCES: 11
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APPLICATION NUMBER:
FILING DATE: 06-JUN-
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TYPE: amino acid
STRANDEDNESS: not releva
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CITY: Boston
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                                                                                                                                                         SGGPLVCDETLQGILSWGVYNESPCGSAQHPAVYTQICKYMSWINKVIRSN 291
                                                                                                                                                                                                                            AGWGTTAARRYKYNKGLTCSSITILSPKNESECEVFYPGVVTNIMICAGLDRGQDPCQSD
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Egelrud,
Hansson,
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Lennart
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Pred. No. 3.1e-140;
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        CITY: Palo Alto
                           STREET:
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; MOLECULE TYPE: protein US-08-557-146-2
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Patent No. 5962300
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Best Local Similarity
                                                                                                                                                             GENERAL INFORMATION:
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TELEPAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
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COMPUTER READABLE PORM:
MEDIUM TYPE: Flogby disk
COMPUTER: IND PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PLENGTI REAGE #1.0, Version #1.25 (EPO)
APELCATION UNFA: 48-086-597,146
FILING DATE: 14-DEC-1995
                                                          APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
TOPOLOGY: linear:
LECTE -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                           229 PNDPGVYTQVCKFTKWINDTMKKH 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 TILSPKBÇEVEYPGVVTNIMIÇAGL-DRGQDPÇQSDSGGPLYCDETLQGILSWGVYPCGS 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 VLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQGEQLRRTTRSVVHPKYHQGSGPILPRRT 133
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is: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.7%; Score 549; DB 2; Length 253; 40.9%; Pred. No. 1.2e-48;
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US-09-154-344-2
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                                                                                                                                               Sequence 2. Application US/09154344
Patent No. 5901256
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Education Torbjorn
APPLICANT: Hamsson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: INCOMPAGE (SCCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query March 36.7%; Score 549; DB 2; Length 253;
Best Local Similarity 40.9%; Pred. No. 1.2e-48;
Matches 108; Conservative 45; Mismatches 97; Indels 14;
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OPERATING SYSTEM: DO
SOFTWARE: FRANSED for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/824,874
FILING DATE: Filed Herewith
CLASSIFICATION WIND: S14
PRIOR APPLICATION MORE:
PRIOR APPLICATION MORE:
PRIOR APPLICATION MORES:
PRILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXQUENCE CHARACTERISTICS;
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDWESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOMEDIATE SOURCE:
LIERRAY: GenBank
CLONE: 532504
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INFORMATION FOR SEQ ID NO: 3:
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NAME: BILLINGS, Lucy J.
REGISTRATION NUMER: 35,749
REFERENCE/DOCKET NUMERS: PF-0
TELECOMMUNICATION : TOPORMATION:
TELEPHONE: 415-855-0555
STREET: 111-
STREET: New York
CITY: New York
                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
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MEDIUM TYPE: Diskette
                                                                                                                                 NUMBER OF SEQUENCES:
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ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 TILSPKECEVFYPGVVTNNMICAGL-DRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGS 252
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                                                                                                                                                                                                                                                                                                                                                                                                 229 PNDPGVYTQVCKPTKWINDTMKKH 252
                                                                                                                                                                                                                                                                                                                                                                                                                          253 AQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 HVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFPSDLMCVDV 168
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COMPUTER READABLE FORM:	XX.	STREET: Lilly Corporate Center CITY: Indianapolis	PONDENCE ADDRESS:	TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS	Johnsto Little,	LICAN	Sequence 2, Application US/08930188 Patent No. 6093397	188-2	229 PNDBGVYTQVCKFTKWINDTWKKH 252	253 AQHPAVYTQICKYMSWINKVIRSN 276	169 KLISPODCTKVYKDILENSMICAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQ 228	194 TILSPKECEVETYPGVVTNNMICAGL-DRGQDPCQSDSGGGLVCDETLQGILSWGVYPCGS 252	109 HVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGMGTTTSPDVTFPSDLMCVDV 168	ki ar pvv pg pryral qi pyr caq pg dq cqya	58 VLYNERWYLTAAHCKWNEYTVHLGSDTLGDRRAQRI-KASKSFRHPGYSTQT 108	QSWVLTAAHCGNKPLWARVGDDHLLLLQG	2 ARSILLPLQILLISTALETAGEEAQGDKIIDGAPCARGSHPWQVALLSGNQLHCGG 57	14 ARALAKILELIMAQIMAABAALLEQNETRIDEBAYGAECARGSQEWQVSLENGISEHCAG 73	Query Match 36.7%; Score 549; DB 2; Length 253; Best Local Similarity 40.9%; Pred. No. 1.2e-48; Matches 108; Conservative 45; Mismatches 97; Indels 14; Gaps 4	ERNOTH: 253 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein -154-344-2	CHARACTERISTICS:	(212) 35 R SEO II	TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 819-8783	REGISTRATION NUMBER: 35,372 REFERENCE/DOCKET NUMBER: 1103326-181	FORMAT:	1-DEC-1995	PRIOR APPLICATION NUMBER: US 08/557,146	SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25 (EPO) CURRENT APPLICATION DATA:	s-Dos	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	ZIP: 10036-2787

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Patent No. 6197511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: La1, Preeti
APPLICANT: La1, Preeti
APPLICANT: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
NOLECULE TYPE: prote
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PILING DATE: 04-RFR-1395
ATTORNEY/AGENT INFORMATION:
NAME: Blaid-lock, Donas K.
REGISTRATION NUMBER: 35/02/
PERCENENCE/JOCKET NUMBER: 35/02/
TREGENOM/INICATION INFORMATION:
TREGENOM/INICATION INFORMATION:
TREGENOM/INICATION INFORMATION:
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                                                               MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                          COUNTRY: U
                                                                                                                                                  STREET: 3174 Po:
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/930,188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 PNDPGVYTQVCKFTKWINDTMKKH 252
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                                                                                                                              USA
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RESULT 14
US-09-764-762-3
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.7%; Score 549; DB 3
Best Local Similarity 40.9%; Pred. No. 1.2e-48;
Matches 108; Conservative 45; Mismatches 97.
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NAME: BILLINGS, LACY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-CTELECOMMUNICATION INPORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BNGTH:
         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL KALLIKREIN
                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 DEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 PNDPGVYTQVCKFTKWINDTMKKH 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 KLISPODCTKVYKDILENSMICAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQ 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 HVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFPSDLMCVDV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 VLVNERWVLTAAHCKMNEYTVHLGSDTLGDRRAQRI-KASKSFRHPGY-----STQT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 VLVDQSWVLTAAHCGNKFLWARVGDDHLLLLQGEQLRRTTRSVVHFKYHQGSGFILFRRT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 ARALAKLIPLIMAQIMAAEAALLPQNPTRLDPEAYGAPCARGSQFWQVSLFNGLSFHCAG 73
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APPLICATION NUMBER: US/09/764,762
                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                         STATE: CA
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PCT-US96-04294-2
                                                                                                                                                                                                                                                                                                 Sequence 2: Application PC/TUS9604294

GRIERAL INVOCAMENCE Eric P.
APPLICANT: Dixon, Eric P.
APPLICANT: Dixon Belanced M.
APPLICANT: Dixon Belanced M.
APPLICANT: DIXON BANACO PROTEIN PROTEASE AND TITLE OF INVESTICAL RELATED NUCLEIC ACIDS

TITLE OF INVESTICAL RELATED NUCLEIC ACIDS

THE OF THE PROTEINS AND THE PROTEINS AND TITLE OF INVESTICAL RELATED NUCLEIC ACIDS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
         ZIP: 46285
COMPUTER READBALE FORM:
MEDILM TYPE: Flogy disk
MEDILM TYPE: Flogy disk
ONEWITE: IN PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTMARE: PASCHIL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                            COUNTRY:
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REGISTRATION WIMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECHMONE: 195-0850-0850
TELECHMONE: 195-385-0850
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: <Unknown>
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                                                                                                                                                                                  Indiana
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                                                                                                                                                               United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US O
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: X9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                               169 KLISPQDCTKVYKDILENSMICAGIPDSKKNACNGDSGGPIVCRGTLQGIVSWGTFPCGQ 228
                                                                                                                                                                                                             134 DEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSI 193
                                  253 AQHPAVYTQIÇKYMSWINKVIRSN 276
                                                                                                                         194 TILSPKECEVFYPGVVTNNMICAGL-DRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGS
                                                                                                                                                                      109 HVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFPSDLMCVDV 168
                                                                                                                                                                                                                                                          58 VLVNERWYLTAAHCKWNEYTVHLGSDTLGDRRAQRI-KASKSFRHPGY-----STQT 108
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                                                                                                                                                                                                                                                                                                                                             2 ARSLLLPLQILLLSTALETAGEEAQGDKIID----GAPCARGSHPWQVALLSGNQLHCGG
PNDPGVYTQVCKFTKWINDTMKKH 252
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Gaps

57

252

Search completed: November 25, 2003, 09:09:43
Job time : 25 secs

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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
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Maximum Match 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                            Score
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Gapop 10.0 , Gapext 0.5
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1496
1 MRAPHLHLSAASGARALAKL......AVYTQICKYMSWINKVIRSN 276
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November 25, 2003, 07:29:59; Search time 51 Seconds
858.991 Million cell updates/sec
                                                                                                                            Match
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                            Length
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            AAW07620
AAB21327
ABG96356
AAU82729
ABP42175
AAB21304
AAB214032
AAB24428
                                                                                                                                                                  SUMMARIES
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Human ovarian canc
Amino acid sequenc
Human ovarian anti
Human KLK-15 prote
Human PRO1303 prot
Human PRO1303 (UNQ
                                                                                                                            Description
                                                                                      Human NES1 polypep
Human NES1. Homo
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	35.2 257	35.6 225 22	35.8 249	36.0 288 22	36.0 288 21 AAB3	36.0 260	36.0 315 23	36.0 306	36.0 305 20	36.0 260 20	36.1 275 21	36.6 260 24	36.6 260 24	36.6 260 24	36.6 260 24	36.6 260 23	36.6 260 23	36.6 260 23	36.6 260 22	36.6 260 22	36.6 260 22	36.6 260 21	36.6 260	6 260 21	36.6 260 20	36.6 260 20	36.6 260 20	36.7 253 24 ABU0747	36.7 253 24	36.7 253 23 AAU8274	36.7 253	36.7 253 23	49 36.7 253	49 36.7 253 16	37.7 248 22 AAB6614	64 37.7 248 22
	Human HSCEE. Homo	Human Stratum Corn		Amino acid sequenc	e o	n serine pr	Human ovarian anti		Human serine prote	Human protease HUP	Human neuropsin.	Human PRO322 polyp			Human PRO polypept		Human PRO322 prote	Human anglogenesis	Human angiogenesis		Novel human diagno	neurops	Human PRO322 (UNQ2	G	Amino acid seguenc	æ			dif	Amino acid sequenc	Human SCCE protein				Protein of the inv	encod

## ALIGNMENTS

RESULT 1
AAW07620
ID AAW0
XX
AC AAW0

AAW07620 standard; Protein; 276 AA

AAW07620;

28-FEB-1997 (first entry)

w	E Human NES1 polypeptide.			
~	*			
*	W NES1; malignancy; cancer; breast carcinoma; cervix carcinoma;	a; cervix	carcinoma;	•
*	W prostate carcinoma; therapy; diagnosis; prognosis; serine protease.	rognosis;	serine pro	otease.
×				
w	s Homo sapiens.			
×				
z	N WO9639175-A1.			
×	*			
0	D 12-DEC-1996.			
×	*			
71	F 21-MAY-1996; 96WO-US07343.			
×	*			
70	R 06-JUN-1995; 95US-0467155.			
×	*			
×	A (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.	S INC.		
×	×			
<b>H</b>	I Band V;			
×				
7	K W/L; 199/-042855/04.			
70	R N-PSDB; AAT44111.			
×	*			
н	T NES1 polypeptide, negatively associated with epithelial cell	ith epith	elial cell	
н	T malignancy - provides diagnostic marker for breast, cervical and	or breast	cervical	and

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RESULT 2
AAB21327
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Best Local :
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                                        WPI; 2000-587440/55
                                                                                                                                                                                                                                                                                                                                                                                       Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; NES1
normal epithelial cell-specific 1; kallikrein-like protein;
New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
                                                                                                              (MOUN ) MOUNT SINAI HOSPITAL
                                                                                                                                                 21-JUL-1999;
                                                                                                                                                                   11-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                          09-MAR-2000; 2000WO-CA00258.
                                                                                                                                                                                                                                                                14-SEP-2000
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                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                      protease; cytostatic; cancer; prostrate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRAPHLHUSAASGARALAKILPILMAQUMAABAALLPQNDTRIDDEAYGAPCARGSQPWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 AA;
                                                                           Diamandis
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                                                                                                                                              99US-0124260.
99US-0127386.
99US-0144919.
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Pred. No. 3.5e-133;
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Best Local Sim
Matches 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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GILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN
                                               GILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                   RVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQ
                                                                                                                                                                                                       RVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQ
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Pred. No. 3.5e-133;
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276

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ABG96356 standard;
Protein;
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11-DEC-2002 ABG96356; (first entry)

Human ovarian cancer marker OV32.

Human; ovarian cancer; macker; concer; familial history, brain disorder; central nervous system disorder; baccerial meningitis; vxxal meningitis; Alzheimer's disease; parkinson's disease; corebral oedems; bydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nonuberquious granulomatous orchitis; connective tissue disorder; insert disease; atherotelacrois; neoplasm;

histological type; carcinogenic;

Homo sapiens

WO200271928-A2

19-SEP-2002

14-MAR-2002; 2002WO-US07826.

14-MAR-2001; 14-MAR-2001; 10-AUG-2001; 19-SEP-2001; 2001US-27602SP. 2001US-276026P. 2001US-311732P. 2001US-323580P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         continuous petient invention relates to a new method for assessing whether a content petient is afflicted with owarian cancer: The method involves comparing the expression level of a marker in a patient sample and the normal level co of expression of the marker in a ontrol non-ovarian cancer sample, where the marker is selected from 50 cancer markers described in the specification. The method of the invention is useful in diagnosing or passible, and the restricted by the presence of cancer as early as content and the restricted by the presence of cancer as early as passible, and the restricted by the presence of cancer as early as conserved and the restricted by the presence of cancer as early as conserved and the restricted by the presence of cancer as early as a cancer. The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial or viral menightis or brain heritations), in the cancer markers of the partitions of the markers of the partitions of control of the control of
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Best Local S
Matches 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assessing whether a patient is afflicted with ovarian cancer, useful in
assessing the stage or progression of the disease, comprises comparing
the expression level of a cancer marker in a sample from a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001; 2001US-324967P.
26-SEP-2001; 2001US-325102P.
26-SEP-2001; 2001US-325149P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 290, 481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from a non cancer patient -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RE,
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                                                                      RVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRQQDPCQSDSGGPLVCDETLQ
                                                                                                                                                                   YHQGSGPILPRRTDBHDIMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAAR
                                                                                                                                                                                                                                                           VSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQGEQLRRTTRSVVHFK
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   GILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                               VSLFNGLSFHCAGVLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQGEQLRRTTRSVVHPK
                                                                                                                                                                                                                                                                                                                        MRAPHLHLSAASGARALAKLLPLLMAQLWAABAALLPQNDTRLDPBAYGAPCARGSQPWQ
                                                                                                                                      YHQGSGPILPRRTDEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAAR
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Moxrisey MP, Olandt PJ, Sen A, Vi
K, Schmandt RE, Zhao X, Glatt X;
                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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Pred. No. 3.5e-133;
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MRAPHLHLSAASGARALAKLL PILMAQLWAAEAALL PQNDTRLDPEAYGAPCARGSQPWQ

60 60 Indels Length 276; 0;

Query Match
Best Local Similarity
Matches 276; Conserv

100.0%; Score 1496; DB 23; ilarity 100.0%; Pred. No. 3.5e-133; Conservative 0; Mismatches 0;

sequence

276 AA;

degeneration. AAU82702-AAU82760 represent the novel human proteases of the invention.

(e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. pretenses and coronary thrombosis) brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. rhemmatoid atthritis and psoriasis) contral and perpenditure of the property of the coronary products of the coronary attention, mood disorders, patchesis, patchesis, property of the coronary products of societies, permission, products of societies, patchesis.

(e.g. Althebiers disease) patching or also useful for trading viral infections caused by human immunodeficiency virus (fry), and non-viral infections such as coular chieses (e.g. glacomal) and menular viral infections such as coular chieses (e.g. glacomal) and menular

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RESULT A AUGUST29 AUG
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treating diseases and disorders such as cancers, immune-related
diseases and disorders, cardiovascular disease (e.g. restenosis) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; processe; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain mood disorder; bypertension; psychotic disorder; psychinesia; vital infection; human immunodeficiency virus; HTV; non-vital infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the isolation of novel human protesses, and the nucleic acids encoding then. The sequences of the invention are useful for treating diseases and disorders such as the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Fig 2K; 313pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-139913/18.
N-PSDB; ABK31771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disorders
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RESULT 5
ABP42175
ID ABP4
The invention relates to 21% novel human ovarian antigens (AB241054-AB24228) and to coDNs encoding them (AB25411)-AB262805), and also encompasses polypeptides 90% identical and polymuclactides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and hose cells comprising human ovarian antigen polymuclactides, antibodies separate human posticus entipsignosis of the reverse properties of the condition of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ovariah cancer, besst cancer; tumour; reproductive system disorder; infactility, prespancy disorder; amountation; polyvystic ovary syndrome; pross, ovarian cyst; dysmanorinosa; endocrine disorder; infaction; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; cardiovascular disorder; urinary system disorder; drug creening; gastroinfestial disorder; urinary system disorder; drug creening; gene blarapy; chromosome maphing; forensic analysis; encorp gene blarapy; chromosome maphing; forensic analysis; encorp in a constraint of the constraint of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reolated mucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of concer (e.g. ovarian concer), immune disorders, cardiovascular disorders and
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# AAB21304; AAB21304 standard; Protein;

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02-FEB-2001 Homo sapiens. prostrate Human, KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; Human KLK-L5 protein #4. kallikrein-like protein; serine protease; cytostatic; cancer;

21-JUL-1999; 01-APR-1999; 11-MAR-1999; 09-MAR-2000; 2000WO-CA00258. 14-SEP-2000 WO200053776-A2 99US-0124260. 99US-0127386. 99US-0144919.

Yousef GM, (MOUN ) MOUNT SINAI HOSPITAL Diamandis

WPI; 2000-587440/55

N-PSDB;

AAA95944.

New kallikrein-like (KLK-L) protein mediated disorders, especially cancer. proteins for diagnosing and treating ZEX-F

Claim 12; Page 172; 184pp; English

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ARESULT ARESTUCT AREA (1) AREA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 118; Conserv
WPI; 2000-594320/56.
N-PSDB; AAC58114.
                                                                                    Botstein D,
                                                                                                                                                                                                                                                                                       08-MAR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; tumour; diagnosis; neoplastic disease; proliferation; cancer; identification; tumourigenesis; anticancer; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO1303 protein sequence SEQ ID NO:33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB24032 standard, Protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of four alternatively spliced kallikrein-like proteins encoded by the human KK-L4 ones, Kallikreins and kallikrein-like proteins are a subgroup of the lateriar brockess enzyme family. They caralyse the selective cleavage of special scruly; Nucleic acids encoding hallikrein-like proteins KK-L1, State acids the teament, montoring and disposis of concurs engage like proteins account of the concern flav can also be used to identify a substancial in the with or redistate the biological activity of the proteins Anthoxies can be used to treat conditions mediated by the kallikrein-like proteins.
                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                  30-NOV-1999
                                                                                                                                                                                                                                                        29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 LKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTAAHCGNKELWARVGEDHLLLLQ-GEQLERTTRSVVHPKYHQGSGEILPERTDEHDLWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLMAQLWAAEAALLPQNDTRLDPEAY-GAPCARGSQPWQVSLPNGLSFHCAGVLVDQSWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHGVYPGRITSNMVCAGGVPGQDACQGDSGGFLVCGGVLQGLVSWGSVGFCGQDGIFGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRIRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPPPDLLQCLNLSIVSHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQIÇKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        СЕМЕХЪСИТИМИТСЯСТВИСОВЬСОВВЕСТИСТВИТЕЛЬНИКИ - VYPCGSAQHPAVY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-----TSHEHDLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLCVLGLSQAA-----TPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 AA;
                                                                               Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                   99WO-US05028.
99WO-US20111.
99US-0162506.
                                                                                                                                                                                              99WO-US28313
99WO-US28634
                                                                                                                                                                                                                                                                                                                                                                       99WO-US28551.
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                                                                               Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                               AL,
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                                                                               Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                               Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                           Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                               H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
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Query Match

Length 248;

Sequence

248 AA;

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Comparison the present invention describes an antibody that binds to a human correction (I) selected from: PROMSI; PROLIS; PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibodies specific for PRO polypeptides, used to diagnose and
the growth of tumors in mammals, and to identify inhibitors of
polypeptide activity or expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 61; Fig 24; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO
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## Matches 1 260 172 201 141 LKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKE 118; 58 LTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-----TSHEHDLRL 111 82 LTAAHCGNKPIWARVGDDHJLLLQ-GEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDIML 140 23 LLMAQLWAAEAALLPQNDTRLDPEAY-GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWV 7 Similarity TYICKYVDWIRMIMRNN 248 CEVFYPGVVINNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWG-VYPCGSAQHPAVY LRIRLPVRVTSSVQPIPIPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHAT 171 LLLCVLGLSQAA-----TPKI FNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWV TQICKYMSWINKVIRSN 276 CHGVYPGRITSNMVCAGGVPGÓDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVY 37.7%; Score 564; DB 21; ilarity 45.9%; Pred. No. 3.9e-45; Conservative 29; Mismatches 92; 92; Indels 18; Gaps 231 81 57

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AAB24428 standard; Protein; 248
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Human PRO1303 protein sequence SEQ ID NO:203.

07-NOV-2000

(first entry

RESULT 8
ANBEZ ATE
ACC ANB
ACC AND
ACC ANB
ACC AND
ACC Human: PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic proliferative; cardiant; cardiovascular; antiatherosclerotic cytostatio; gene therapy; vaccine.

Homo sapiens.

WO200032221-A2

08-JUN-2000

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The present invention describes nucleic acids encoding PRO polypeptides cardiovascular, endothelial or angiogenesis and creating diagnosing a cardiovascular, endothelial or angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with the cinappropriate PRO expression such as excitovascular, andothelial or angiogenic disorders in mammals (e.g. atherosciacular, andothelial or angiogenic disorders in mammals, e.g., atherosciacular, andothelial or angiogenic disorders in mammals, e.g., atherosciacular, andothelial or cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polymeptide may be used to treat disorders containing them and the PRO polymeptide may be used to treat disorders containing them and the PRO polymeptide may be used to treat disorders and AA2138 to AAA2135 represent nucleotide and protein sequences used in the exemplification of the present throation.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-1999;
23-JUN-1999;
20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 72; Fig 82; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-412154/35.
N-PSDB; AAA77671.
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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12-JAN-1999;
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                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                    23 LLMAQLWAAEAALLPQNDTRLDPEAY-GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWV
                      CHGVYPGRITSNNVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVY
                                                                                                                                            LKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKE
                                                                                                                                                                                                            LTAAHCSGSRYWVRLGEHSLSQLDWTEQIKHSGFSVTHFGYLGAS-----TSHEHDLRL
                                                                    CEVFYPGVVTNNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWG-VYPCGSAQHPAVY 259
                                                                                                                 LRLRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHAT 171
                                                                                                                                                                                                                                                          LTAAHCGNKPLWARVGDDHLLLLQ-GEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLML 140
                                                                                                                                                                                                                                                                                                       LLLCVLGLSQAA-----TPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney AL, K
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0111445
99US-0114287
99WO-US12252
99US-0141037
99US-0144758
99US-0144758
99WO-US20111
99WO-US2011
99WO-US2014
99WO-US2014
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99WO-US05028.
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                                                                                                                                                                                                                                                                                                                                                                                                                            37.7%; Score 564; DB 21; Length 248; 45.9%; Pred. No. 3.9e~45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrara N, Gerber H, Hillan KJ, Godd Klein RD, Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                                      29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                  92; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard A;
                                                                                                                                                                                                            111
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A AV89939

A AV89939

A AV89939

A AV89939

A AV89939

A AV893939

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                  18-SEP-1998
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10-SEP-1998;
10-SEP-1998;
15-SEP-1998;
15-SEP-1998;
15-SEP-1998;
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09-SEP-
09-SEP-
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10-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY99393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY99393 standard; Protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQICKYMSWINKVIRSN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                  98US-0101068

98US-0101071

98US-0101471

98US-0101471

98US-0101472

98US-0101474

98US-0101475

98US-0101477

98US-0101477
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98US-0100849.
98US-0101014.
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98US-0100662

98US-0100683

98US-0100684

98US-0100710

98US-0100711

98US-0100930
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98US-0100390.
98US-0100584.
98US-0100627.
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98US-0099763.
98US-0099792.
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98US-0098843.
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Best Local Simi
Matches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
                                                                                                                                                                                                                                                                                                                                         Sequence
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N-PSDB; AAA37075.
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                                                                                                                                                                                                                                  LLMAQIWAABAALLEQNDTRLDPEAY-GAPCARGSQPWQVSLFNGLSFHCAGVLVDQSWV
    TOICKYMSWINKVIRSN
                            CHGVYPGRITSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSNGSVGPCGQDGIPGVY
                                                  CEVFYPGVVINNMICAGLDRGQDPCQSDSGGPLVCDETLQGILSWG-VYPCGSAQHPAVY
                                                                                          LRLRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHAT
                                                                                                                                                    LTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGESVTHPGYLGAS-----TSHEHDLRL
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ilarity 45.9%;
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98US-0108904.
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Pred. No. 3.9e-45;
9; Mismatches 92;
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TYICKYVDWIRMIMRNN

AAM23994 standard; Protein; 248

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AAM23994;

12-OCT-2001 (first entry)

Human EST encoded protein SEQ ID NO: 1519.

RESULT 10
ANN2394
ID ANN2395
XX
AC ANN23
XX
II 12-OC
XX
Humar
XX
H Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomatc; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.

Homo sapiens

WO200154477-A2

02-AUG-2001

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RESULT 11
ANB66142
ID AAB66142
ID AAB66
XX AC AAB66
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17-JUL-2000;
03-AUG-2000;
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                                    Unidentified
            WO200078961-A1
                                                          Secreted;
                                                                                Protein of the
                                                                                                        02-APR-2001
                                                                                                                                                    AAB66142 standard;
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                                                                                                                                                                                                                                                                                                                                                LTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-----TSHEHDLRL
                                                        transmembrane; gene therapy.
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2000US-0617746.
2000US-0631451.
2000US-0663870.
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A, Zhang
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45.9%;
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J, W
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Pred. No. 3.9e-45;
9; Mismatches 92;
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Query Match
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Matches 118
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16-DEC-1999;
05-JAN-2000;
06-JAN-2000;
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26-JUL-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                            Gao W,
                                                                            The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense BNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The muclair acids may also be used in gene therapy.
                                                    Sequence
                                                                                                                                                                                      Claim 1; Fig 108; 787pp; English.
                                                                                                                                                                                                                 therapy
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            Local Similarity 45.9%;
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Goddard A, Godowski PJ, Grimaldi CJ, G,
Paoni NF, Roy MA, Smith V, Stewart TA,
abe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                               ) GENENTECH INC
                                                    248 AA;
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2000WO-US00376.
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99WO-US28551.
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99US-0145698.
99WO-US20111.
Score 564; DB 22;
Pred. No. 3.9e-45;
9; Mismatches 92;
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TA, Tumas D;
                         Length 248;
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Hillan KJ;
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RESULT 12
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AAR67888 standard; Protein; 253
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25-MAR-2003 09-AUG-1995

(updated) (first en

entry)

AAR67888;

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RESULT 13
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               31-DEC-1996
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                                           AAW05383;
                                                                        AAW05383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid p8507. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, specially to treat and prevent can, exercderms, or other hyperkeratoric conditions (e.g. callosities or keratosis pilarys); inchiposes; postissis, eccement, etc. It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 97; 137pp; English
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                                                                        standard;
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                                                                                                                                                                                                                                                             HVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFPSDLMCVDV
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                                                                                                                                              PNDPGVYTQVCKFTKWINDTMKKH 252
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                                                                                                                                                                                                    KLISPQDCTKVXXDLLENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hansson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
               (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corneum chymotrophic recombinant enzyme (SCCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93DK-0000725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-IB00166
                                                                        Protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                  36.7%; Score 549; DB 1
40.9%; Pred. No. 1e-43;
tive 45; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                     97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chymotryptic enzyme polypeptides, or psoriasis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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RESULT 14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        himan amyloid precursor protein protease (hAMOS383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid psptide. Its amino acid sequence was deduced from a cDNA clone (hAMT9788) obt. from a human lung library. Recombinant protease can be produced in transformed or transfered protaryotic (partic. R. coil) or esharyotic (partic. AVI210) best cells. It is used to develop products for the design and testing of cpds useful for treating or preventing conditions associated with beta-amyloid psptide, esp. Alteiner's disease.
                                                  ABB84406;
                                                                               ABB84406 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 44-45; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human amyloid precursor protein protesse - usedevelop prods. for the treatment or disgnosis of associated conditions, esp. Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human amyloid precursor protein protease
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                                                                                                                                                                   229
                                                                                                                                                                                                                                      169 KLISPQDCTKVYKDLLENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQ
                                                                                                                                                                                                                                                                   194 TILSPKECEVEYPGVVTNNMICAGL-DRGQDPCQSDSGGPLVCDETLQGILSWGVYPCGS
                                                                                                                                                                                                                                                                                                     109 HVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFPSDLMCVDV
                                                                                                                                                                                                                                                                                                                                       134 DEHDLMLLKLARFVVPGFRVRALQLFYRCAQFGDQCQVAGWGTTAARRVKYNKGLTCSSI 193
                                                                                                                                                                                                                                                                                                                                                                       58 VLVNERWYLTAAHCKMNEYTVHLGSDTLGDRRAQRI-KASKSFRHPGY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 ARALAKLLPLIMAQIWAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSJFNGLSFHCAG
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                                                                                                                                                                                                                                                                                                                                                                                          VLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQGEQLRRTTRSVVHPKYHQGSGPILPRRT
                                                                                                                                                                                                   AQHPAVYTQICKYMSWINKVIRSN 276
                                                                                                                                                                   PNDPGVYTQVCKFTKWINDTMKKH 252
                                                                                                                                                                                                                                                                                                                                                                                                                                       ARSLILPIQILILSLALETAGEEAQGDKIID----GAPCARGSHPWQVALLSGNQLHCGG
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                                                                               Protein, 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.7%; Score 549; Di
40.9%; Pred. No. 1e-4
live 45; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253;
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(first entry)

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Best Local S
Matches 108
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09-FEB-2001; 2001DK-0000218.
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N-PSDB; ABQ76226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 58-59; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression in skin
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                                                                                                                                                                                                                             Local Similarity
wes 108; Conserv
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) HANSSON L.
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   DEHDLMLLKLARPVVPGPRVRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSI 193
                                               VLVNERWYLTAAHCKOMEYTVHLGSDTLGDRRAQRI-KASKSFRHPGY-----STQT 108
                                                                                       VLVDQSWVLTAAHCGNKPLWARVGDDHLLLLQGEQLRRTTRSVVHPKYHQGSGPILERRT 133
                                                                                                                                      ARSILLPLQILLSLALETAGEEAQGDKIID----GAPCARGSHPWQVALLSGNQLHCGG 57
                                                                                                                                                                                 ARALAKLIPLIMAQIMAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAG 73
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                                                                                                                                                                                                                                                                                                                        AA,
                                                                                                                                                                                                                                                      36.7%;
                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                Score 549; DB
Pred. No. 1e-4
45; Mismatches
                                                                                                                                                                                                                                                      1e-43;
                                                                                                                                                                                                                                                                            DB 23;
                                                                                                                                                                                                                                97;
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Haman Market Mar
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This invention describes a novel non-human transgenic mammal or mammal and combryon baving integrated within its genome, a heterologous mucleotide sequence comprising at least a significant part of a nucleotide sequence (coding for a stratum content that drives expression of heterologous scee or its variant; and in the product of the invention is useful as a model of or its variant in skin. The product of the invention is useful as a model of commetic or a planmaceutical formulation, for development or treating of a commetic or a planmaceutical formulation, and for the development of a commetic or a planmaceutical formulation, and for the development of a commetic or a planmaceutical formulation, for development or treating of a composition material production of the treating of a composition production effective for the prevention or treatment of an examination or unwanted plannitype, and for acreening or dentifying a compound or composition effective for the prevention or treatment of the hyperkeratoois, acanthosis, epidermal inflammation, dermal inflammation, composition and compositions of the invention is also useful case with epidermal typerkeratoois. The mammal of the invention is also useful case a model for further studies of the mechanisms and the resting of potential compounds and compositions for relieve to traitous skin diseases white epidermal is a compound. This evention is a compound on the section of the control of the c
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09-FEB-2001; 2001DK-0000218.
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(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 HVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFP8DLMCVDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment of the human stratum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLKT) used in the development of the transgenic mammais described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                194 TILSPRECENTEROVYRNANICAGI-BROODCOSSGGPLYCDETLOGILSROVYRCGS 252
                                                                                                                                                                                                                             134 DEHDLMILKLARPVVPGPRVRALQLPVRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSI 193
                                                                                                                                                                                                       109 HVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFPSDLMCVDV 168
                                                                                                                                                                                                                                                                             58 VLYNERWYLTAAHCKGNEYTVHLGSDTLGDRDAQRI-KASKSFRHFGY-----STQT 108
                                                                                                                                                                                                                                                                                                      74 VLVDQSWVLTAAHCGNKELMARVGDDHLLLLQGEQLRRTTRSVVHPKYHQGSGPILPRRT 133
                                                                                                                                                                                                                                                                                                                                                   14 REALKLIPLIAGUMAARALLEQNITRUDFEAYGAFCARGSOPHQVSLFNGLSEHCAG 73
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